

(TM)

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n.a. database search, using Smith-Waterman algorithm

Tue Aug 3 18:01:42 1999; MasPar time 546.13 Seconds

t generated.

I    ATCCCATCTGAGCCTCCCTGAG...GTCAGGAAGGCCGATACCTCTT    20  
TCGGTGACGTGAGGGACTC...CAGGTCTTCGGCTTTGAGAA

TABLE default

```

phase 0; Query 0

```

2883791 seqs, 1171580779 bases x 2

Minimum	Match 0%
Listing first	45 summaries

```
6:em_est19 //:em_gss1
genbank-est111
```

34:qb\_esc/ 35:qb\_esc8 36:qb\_esc9 37:qb\_gss1 38:qb\_gss2  
39:qb\_gss3 40:qb\_gss4 41:qb\_gss5 42:qb\_gss6

mean 9.722; Variance 2.315; scale 4.199

ved by analysis of the total score distribution.

## SUMMARIES

8.3	AI39114/	mcibg01.y1	Soares	1.8/e-119
26	AI323091	mj73b06.y1	Soares	1.87e-119
25			Soares	1.87e-119

Accession	Gene	Protein	Accession	Gene	Protein
44	10.7	AF038250	Human	AF038250	Human mRNA (1
45	10.3	AA688510	Barstead	mo	7.89e-09
27	10.3	403 16	Barstead	mo	7.89e-09

## ALIGNMENTS

COMMENT On Sep 12, 1996 this sequence version replaced gi:1394394.

Other\_ESTS: THC104472  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

# FEATURES

source  
 Location/Qualifiers  
 1..274  
 /organism="Homo sapiens"  
 /note="Organ: uterus; Vector: pBluescript SK-; Site\_1:  
 EcorI; Site\_2: XhoI"  
 /db\_xref="ATCC (Inhost):192971"  
 /db\_xref="taxon:9606"  
 /clone\_lib="uterus tumor I"  
 /dev\_stage="adult"  
 ORIGIN  
 BASE COUNT 60 a 80 c 84 g 46 t 4 others

Query Match 95.8%; Score 250; DB 11; Length 274;  
 Best Local Similarity 97.7%; Pred. No. 0.00e+00;  
 Matches 252; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 1 CACTGACCTCCCTAGACACTTACAGAGCGGAGACCCAGACATGAGAGGCTCCT 60  
 QY 4 CACTGACCTCCCTAGACACTTCTACAGAGCGGAGACCCAGACATGAGAGGCTCCT 63  
 Db 61 CCGTGACACAGCGCTGGTGTGTCTGTGGGAGGAGGAGTGTAGTCCACGCCAA 120  
 QY 64 CCGTGACACAGCGCTGGTGTGTCTGTGGGAGGAGGAGTGTAGTCCACGCCAA 123  
 Db 121 GGTCCCTATNAGATGCAAGTNAACACTGCGCTCAGAGAGAGCCAGAGAGGCTTG 180  
 QY 124 GGTCCCTATNAGATGCAAGTNAACACTGCGCTCAGAGAGAGCCAGAGAGGCTTG 183  
 Db 181 GGGGCGCCGTTTGGTGGAGCTCCGGAGAGAGGAGCAGCTGGTGTGTCTCCCTGT 240  
 QY 184 GGGGCGCCGTTTGGTGGAGCTCCGGAGAGAGGAGCAGCTGGTGTGTCTCCCTGT 243  
 Db 241 CCAGAGCCGAACTTT 258  
 QY 244 CCAGAGCCGAACTTT 261

RESULT 2  
 LOCUS 772043 378 bp mRNA EST 01-MAR-1995  
 DEFINITION yc63b05.r1 Stragene liver (#937224) Homo sapiens cDNA clone  
 IMAGE:85329 5', mRNA sequence.

ACCESSION T72043  
 NID 9686564  
 VERSION T72043.1 GI:686564  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 378)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,  
 Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.  
 WASHU-Merck EST Project

TITLE Unpublished (1995)  
 JOURNAL  
 COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800

Fax: 314 286 1810  
 Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
 High quality sequence stops: 291  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
 Seq primer: M13RP1  
 High quality sequence stop: 291.

# FEATURES

source  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /note="Organ: liver; Vector: pBluescript SK; Site\_1:  
 EcorI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dt. Hepatectomy from normal male caucasian. Average  
 insert size: 1.1 kb. Uni-ZAP XR Vector; ~5' adaptor  
 sequence: 5' GAATTCGGACGAG 3' ~3' adaptor sequence: 5'  
 CTGACGTTTCTTTTCTTTTCTTTT 3'."  
 /db\_xref="GDB:502386"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:85329"  
 /clone\_lib="Stragene liver (#937224)"  
 /sex="male"  
 /dev\_stage="49 years old"  
 /lab\_host="SOLR cells (kanamycin resistant)"  
 BASE COUNT 83 a 117 c 116 g 59 t 3 others  
 ORIGIN

Query Match 92.3%; Score 241; DB 19; Length 378;  
 Best Local Similarity 97.7%; Pred. No. 0.00e+00;  
 Matches 256; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Db 11 AGCCACTTCAAGCTCCCTGAGACCTCTCTACAGAGCGGAGCCCGACATGAGGAGGC 70  
 QY 1 AGCCACTGCA-GCTCCCTGAGACCTCTCTACAGAGCGGAGCCCGACATGAGGAGGC 59  
 Db 71 TCCCTCTGGTACACAGCCTGCTGTGTCTGTGTGGAGGAGGAGTGCAGTCCAGCAC 130  
 QY 60 TCCCTCTGGTACACAGCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 119  
 Db 131 CCAAGTCCCTATCAAGATGCAAGTCAACATGAGCGCCCTAGAGCAGAGCCAGAGAGG 190  
 QY 120 CCAAGTCCCTATCAAGATGCAAGTCAACATGAGCGCCCTAGAGCAGAGCCAGAGAGG 179  
 Db 191 CCGTGGG-CGCCCGT 249  
 QY 180 CCGTGGGCGCCGCTGT 239  
 Db 250 CTGTCCAGAGCCGAACTTT 271  
 QY 240 CTGTCCAGAGCCGAACTTT 261

RESULT 3  
 LOCUS 778178 424 bp mRNA EST 15-MAR-1995  
 DEFINITION yd79c11.r1 Soares fetal liver spleen INFIS Homo sapiens cDNA clone  
 IMAGE:114452 5', similar to contains PTRS repetitive element ;, mRNA  
 sequence.

ACCESSION T78178  
 NID 9696687  
 VERSION T78178.1 GI:696687  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 424)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and  
 Wilson, R.

TITLE The Mashu-Merck EST Project  
 JOURNAL  
 Unpublished (1995)



REFERENCE 1 (bases 1 to 357)  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 TITLE The WashU-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 Insert Size: 716  
 High quality sequence stops: 232 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 716 Std Error: 0.00  
 Seq primer: M13p1  
 High quality sequence stop: 232.  
 Location/Qualifiers  
 1..357  
 /organism="Homo sapiens"  
 /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site.1: Pac I; Site.2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAGATTAATTAAGATCTTTTATTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."  
 /db\_xref="GDB:470308"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:114691"  
 /clone\_lib="Soares fetal liver spleen INFLS"  
 /sex="male"  
 /dev\_host="20 week-post conception fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 BASE COUNT 72 a 101 c 112 g 64 t 8 others  
 ORIGIN  
 Query Match 64.0%; Score 167; DB 19; Length 357;  
 Best Local Similarity 94.8%; Pred. No. 8,64e-233;  
 Matches 200; Conservative 0; Mismatches 6; Indels 5; Gaps 4;  
 1 AGGCTCCTCTGTGTCACAGCCTGTGTTGCTGTGGGAGGAGGAGTGCAGTCCC 60  
 56 AGGCTCCTCTGTGTCACAGCCTGTGTTGCTGTGGGAGGAGTGCAGTCCC 60  
 61 AGCACCAGGCTCTATCAAGATGCAAGTCAACACTGAGCCCTCAGAGCAGCCAGA 120  
 115 AGCACCAGGCTCTATCAAGATGCAAGTCAACACTGAGCCCTCAGAGCAGCCAGA 174  
 121 GAACAGGCGCTGNGGCGCTGTGGTGGAGCTCCGAGAGAGAGCAGCAGTGGTGG 180  
 175 GAA--GGCTGGGGGCGCCCT-GTGG-TGGAGCCTCCGAGAGAGAGCAGCAGTGGTGG 230  
 181 TGGTGTTCCTGTCCAGAGCCGAACCTCT 211  
 231 TGGTGTTCCTGTCCAGAGCCGAACCTCT 261  
 RESULT 6  
 LOCUS AA502331 534 bp mRNA EST 19-AUG-1997  
 DEFINITION ne26h06.s1 NCI\_CGAP\_C03 Homo sapiens cDNA clone IMAGE:898523 3' similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN. ;, mRNA sequence.  
 ACCESSION AA502331  
 NID 92237298  
 VERSION AA502331.1 GI:2237298

KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 534)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1407178.  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arraying: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrip/image/image.html  
 Insert length: 690 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 398.  
 Location/Qualifiers  
 1..534  
 /organism="Homo sapiens"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization."  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:898523"  
 /clone\_lib="NCI\_CGAP\_C03"  
 /sex="pooled"  
 /tissue\_type="colon"  
 /lab\_host="DH10B"  
 BASE COUNT 80 a 160 c 178 g 115 t 1 others  
 ORIGIN  
 Query Match 61.3%; Score 160; DB 14; Length 534;  
 Best Local Similarity 95.1%; Pred. No. 9,18e-221;  
 Matches 173; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
 354 AAGAGTTTGGCTTGTGAGCAGGAGACAGCACCAGCTGTGCTTCTCCGAGGC 413  
 261 AAGAGTTTGGCTTGTGAGCAGGAGACAGCACCAGCTGTGCTTCTCCGAGGC 202  
 414 TCACACAGGCGGCCCGCCAGGC-TTCTGTGGTCTGCTGAGNGCAGTGTGACT 472  
 201 TCACACAGGCGGCCCGCCAGGCCTTCTGTGCTGAGNGCAGTGTGACT 142  
 473 TCCATCTTGATAGGAACCTTGGTCTGGGATGACCTGCTCCACAGAAAACA 532  
 141 TGCATCTTGATAGGAACCTTGGTCTGGGATGACCTGCTCCACAGCACAACC 82  
 533 AC 534  
 Cp 11  
 Cp 81 AC 80  
 RESULT 7  
 LOCUS AA503839 501 bp mRNA EST 19-AUG-1997  
 DEFINITION ne53a10.s1 NCI\_CGAP\_C03 Homo sapiens cDNA clone IMAGE:901050 3' similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN. ;, mRNA sequence.

ACCESSION AA503839  
NID 92238805  
VERSION AA503839.1 GI:2238806  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 501)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT On Apr 14, 1993 this sequence version replaced gi:693200.

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,  
M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arraying: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LDNL at:  
[www.bio.llnl.gov/bdrp/image/image.html](http://www.bio.llnl.gov/bdrp/image/image.html)

Insert Length: 586 Std Error: 0.00  
Seq primer: -40ml3 fwd, ET from Amersham  
High quality sequence stop: 190.  
Location/Qualifiers

FEATURES  
source

1..501  
/organism="Homo sapiens"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from 12 pooled bulk tumor samples and primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified p773 vector. Library went through one round of  
normalization.  
/db\_xref="taxon:9606"  
/clone="IMAGE:901050"  
/clone\_lib="NCI\_CGAP\_C03"  
/sex="pooled"  
/tissue\_type="colon"  
/lab\_host="DH10B"

BASE COUNT  
ORIGIN

62 a 148 c 165 g 126 t

Query Match 59.4% Score 155; DB 14; Length 501;  
Best Local Similarity 98.1% Pred. No. 3,41e-212;

Matches 158; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 341 AAGAGTTTCGGCTTCTGGACAGGAGACACACACAGCTGCTCTCCGAGGC 400  
|||||  
Cp 261 AAGAGTTTCGGCTTCTGGACAGGAGACACACACAGCTGCTCTCCGAGGC 202  
|||||  
Db 401 TCCACACACGGGGCCCCAGGCTCTCTGGGTCCTGCTGAGGCCAGTGTGACT 460  
|||||  
Cp 201 TCCACACACGGGGCCCCAGGCTCTCTGGGTCCTGCTGAGGCCAGTGTGACT 142  
|||||  
Db 461 TGGATCTTGATGGAGACCTGGGTCCTGGAGCTGCACCTGC 501  
|||||  
Cp 141 TGCATCTTGATGGAGACCTGGGTCCTGGAGCTGCACCTGC 101  
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RESULT 8  
LOCUS AA568450 474 bp mRNA EST 09-SEP-1997  
DEFINITION mm25b08.s1 NCI\_CGAP\_C010 Homo sapiens CDNA clone IMAGE:1061175 3'  
similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN.;', mRNA  
sequence.  
ACCESSION AA568450

NID 92341504  
VERSION AA568450.1 GI:2341504  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 474)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT On Sep 12, 1996 this sequence version replaced gi:1402127.

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,  
M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arraying: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LDNL at:  
[www.bio.llnl.gov/bdrp/image/image.html](http://www.bio.llnl.gov/bdrp/image/image.html)

Insert Length: 651 Std Error: 0.00  
Seq primer: -40ml3 fwd, ET from Amersham  
High quality sequence stop: 197.  
Location/Qualifiers

FEATURES  
source

1..474  
/organism="Homo sapiens"  
/note="Organ: colon. Vector: p773D-Pac (Pharmacia) with a  
modified polylinker. 1st strand cDNA was prepared from  
RER+ colon tumor, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified p773  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo (N-Soares4).  
/db\_xref="taxon:9606"  
/clone="IMAGE:1061175"  
/clone\_lib="NCI\_CGAP\_C010"  
/tissue\_type="colon tumor RER-"  
/lab\_host="DH10B"

BASE COUNT  
ORIGIN

61 a 142 c 157 g 114 t

Query Match 39.8% Score 104; DB 15; Length 474;  
Best Local Similarity 100.0% Pred. No. 4.50e-125;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 371 AAGAGTTTCGGCTTCTGGACAGGAGACACACACAGCTGCTCTCCGAGGC 430  
|||||  
Cp 261 AAGAGTTTCGGCTTCTGGACAGGAGACACACACAGCTGCTCTCCGAGGC 202  
|||||  
Db 431 TCCACACACGGGGCCCCAGGCTCTCTGGGTCCTGCTGTA 474  
|||||  
Cp 201 TCCACACACGGGGCCCCAGGCTCTCTGGGTCCTGCTGTA 158  
|||||

RESULT 9  
LOCUS A1391147 560 bp mRNA EST 02-FEB-1999  
DEFINITION mcl6g01.y1 Soares protein p3NMF19.5 Mus musculus CDNA clone  
IMAGE:348720 5' similar to gb:028486 Mus musculus uterine-specific  
proline-rich acidic protein (MOUSE);', mRNA sequence.  
ACCESSION A1391147  
NID 94217154  
VERSION A1391147.1 GI:4217154  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE 1 (bases 1 to 560)  
 AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 TITLE The WashU-NCI Mouse EST Project 1999  
 JOURNAL Unpublished (1999)  
 COMMENT On Apr 14, 1993 this sequence version replaced gi:716760.

Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 486.  
 Location/Qualifiers  
 1..560  
 /organism="Mus musculus"  
 /note="Vector: p773D (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGGCCGCAATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."  
 /db\_xref="taxon:10090"  
 /map="12"  
 /clone="IMAGE:348720"  
 /clone\_lib="Soares mouse p3NMF19.5"  
 /dev\_stage="19.5 dpc total fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /db\_xref="lab:10090"

BASE COUNT 136 a 162 c 148 g 113 t 1 others  
 ORIGIN

Query Match 38.3%; Score 100; DB 26; Length 560;  
 Best Local Similarity 73.4%; Pred. No. 1.87e-119;  
 Matches 157; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Db 44 CCCAGCATGAAGAGTTTCTCTGCGCAGCTTTGGTGCTGCACCTGCTGGAGG 103  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 42 CCCAGCATGAAGAGTTTCTCTGCTGCTGCACCTGCTGGTGCTGCTGGAGG 101  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 104 CAGCGCAGCTCCAGCAGCAGCAGCTCCCTGTCAGACCAAGCAATGTTCCTG 163  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 102 CAGGTGCACTCCAGCAGCAGCAGCTCCCTGTCAGATGCAAGTCAAACTGCGCCCTGAG 161  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 164 AACAGGAACAGAGAGTGTGGATCTAGAGCCCTGAGAGCTCTGAAAGAGCAACC 223  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 162 AGCAGGACCCAGAGAGAGGCTGGGGGCCCGGTGTGTGAGAGCCCTCGGAGAGAGAGCAGC 221  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 224 AGCTGGGGCCACTGCTCTCTGAACCCCAACAGAA 257  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 222 AGCTGTGTGTGTCTCTCTGTCAGAAAGCCGAA 255

RESULT 10 A1323091 590 bp mRNA EST 23-DEC-1998  
 LOCUS m73b06.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone  
 DEFINITION IMAGE:481715 5' similar to gb:028486 Mus musculus uterine-specific proline-rich acidic protein (MOUSE);, mRNA sequence.

ACCESSION A1323091  
 MID 94057520  
 VERSION A1323091.1 GI:4057520  
 KEYWORDS EST  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 590)  
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowers, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
 TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT On Apr 14, 1993 this sequence version replaced gi:693536.

Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 444.  
 Location/Qualifiers  
 1..590  
 /organism="Mus musculus"  
 /note="Vector: p773D (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGGCCGCAATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."  
 /db\_xref="taxon:10090"  
 /map="between D1S1765 and UGB"  
 /clone="IMAGE:481715"  
 /clone\_lib="Soares mouse p3NMF19.5"  
 /dev\_stage="19.5 dpc total fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /db\_xref="lab:10090"

BASE COUNT 152 a 167 c 151 g 118 t 2 others  
 ORIGIN

Query Match 38.3%; Score 100; DB 25; Length 590;  
 Best Local Similarity 73.4%; Pred. No. 1.87e-119;  
 Matches 157; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Db 46 CCCAGCATGAAGAGTTTCTCTGCGCAGCTTTGGTGCTGCACCTGCTGGAGG 105  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 42 CCCAGCATGAAGAGTTTCTCTGCTGCTGCACCTGCTGGTGCTGCTGGAGG 101  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 106 CAGCGCAGCTCCAGCAGCAGCTCCCTGTCAGACCAAGCAACACTGTTCCTG 165  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 102 CAGGTGCACTCCAGCAGCAGCAGCTCCCTGTCAGATGCAAGTCAAACTGCGCCCTGAG 161  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 166 AACAGGAACAGAGAGTGTGGATCTAGAGCCCTGAGAGCTCTTGAAGAGCAACC 225  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 162 AGCAGGACCCAGAGAGAGGCTGGGGGCCCGGTGTGTGAGAGCCCTCGGAGAGAGCAGC 221  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 226 AGCTGGGGCCACTGCTCTCTGAACCCCAACAGAA 259

OY	222	AGCTGTCGTCTGTTCCCTGTCACGAAGCGCAA	255			
RESULT	11					
LOCUS	M36494	578 bp	mRNA EST 11-SEP-1996			
DEFINITION	M36494.1 Soares mouse p33MF19.5 Mus musculus cDNA clone IMAGE:334915 5' similar to gb:U28486 Mus musculus uterine-specific proline-rich acidic protein (MOUSE).; mRNA sequence.					
ACCESSION	W36494					
NID	g1318399					
VERSION	W36494.1 GI:1318399					
KEYWORDS	EST.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Mammalia; Eutheria; Rodentia; Scurionathii; Muridae; Murinae; Mus.					
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Teisling,B., Wille,I., Lennon,G., Soares,B., Wilson,R. and Waterston,R.					
TITLE	The Mashu-HMI Mouse EST Project					
JOURNAL	Unpublished (1996)					
COMMENT	On Nov 29, 1993 this sequence version replaced gi:430545.					
<hr/>						
Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (infoimage.lnl.gov) for further information. MGI:216315 Seq primer: ETPRimer High quality sequence stop: 401. Location/Qualifiers						
FEATURES	SOURCE					
	1..578					
	/organism="Mus musculus"					
	/note="Vector: pRTT3D (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTCACATCTGAAGTGCGAGCGGCCGCATTCTTTTTTTTTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)." /db_xref="taxon:10090"					
	/map_xref="21"					
	/clone="IMAGE:334915"					
	/clone_lib="Soares mouse p33MF19.5"					
	/dev_stage="19.5 dpc total fetus"					
	/lab_host="DH10B (ampicillin resistant)"					
BASE COUNT	143 a	155 c	159 g 114 t 7 others			
ORIGIN						
Query Match	37.2%	Score 97:	DB 34; Length 578;			
Best Local Similarity	73.8%;	Pred.	No.1,65e-114;			
Matches	158: Conservative	0: Mismatches	55: Indels 1: Gaps 1:			
Db	44	CCCCAGTATGAAGAGGTTCTCTCTGGCCACTGTTTGTCGTCACCTGCTGTGGAGG	103			
OY	42	CCCCAGACATGAGGAGGCTCTCTGTCGTCACCAGCGCTGCTGTCGTCGTGGAGG	101			
Db	104	CAGGGCAGGTC-CACCAKCCAGGTCCTGTCACGACCAAGCAACAACATGTTTCCCG	162			
OY	102	CAGGTCAGCTCCACACGCCAAGGTCCTCATTAAGAATGCAAACTCAACACTGACCTTAG	161			

Db	163	AACGAGAAACAGAGAGAGCTGTGCGATACGAGCCCTGCTTGAAGAGCAAC	222
Y	162	AGCAGAGACCCAGAGAGAGGCTTGGGAGCCCTGTGTGTGAGACTTCGAGAGAGCAGC	221
Db	223	AGCTGGGGCCACTGCTTCTGTACCCCAACAGAA	256
Y	222	AGCTGTGTGTCTGTCTTCCCTTCCAGAGCCGAA	255
RESULT	12		
LOCUS	W10974	600 bp	mRNA
DEFINITION	ma46d11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone		EST
ACCESSION	W10974		01-OCT-1997
NID	91285279		
VERSION	W10974.1		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 600) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B., Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.		
TITLE	The Mashu-HHMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI: 204365 Seq primer: ETPRimer High quality sequence stop: 477.		
FEATURES	Location/Qualifiers		
Source	1..600		
	/organism="Mus musculus"		
	/note="Vector: pY713D (Pharmacia) with a modified polylinker. Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dn) primer 15', TGTTACCAATCTCAAGTGGAGGCGCCGCAATTTTTTTTTTTTTTTT 3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pY713 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."		
	/db_xref="taxon:10090"		
	/clone_xref="IMAGE:313749"		
	/clone_lib="Soares mouse p3NMF19.5"		
	/dev_stage="19.5 dpc total fetus"		
	/lab_host="DH10B (ampicillin resistant)"		
BASE COUNT	165 a 161 c 155 g 119 t		
ORIGIN			
Query Match	37.2%	Score 97;	DB 33; Length 600;
Best Local Similarity	73.8%;	Pred. No. 1,65e-114;	
Matches	156; Conservative	0; Mismatches 55;	Indels 1; Gaps 1;
Db	27	CCCCGATCATGAAGAGTTTCTCTGCGCAGCTGTGTGTCGACATGCTGTGGAGG	86
Y	42	CCCCGAGATATGAGAGGCTCTCTGTCGACACAGCGTGTGTGTGCTGTGTGGAGG	101

Contact: Maira M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 MGI:218688  
 Seq. primer: EMP1mer  
 High quality sequence stop: 388

BASE COUNT	ORIGIN
245 a	217 c
420 g	215 t
	17 others

Query Match	37.28;	Score 97;	DB 34;	Length 1114;
Best Local Similarity	73.88;	Pred. No. 1.65e-114;		
Matches	158;	Conservative	0;	Mismatches 55;
			Indels	1;
			Gaps	1;

Contact: Marra M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel.: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LINL; contact the  
IMAGE Consortium (info@image.linn.gov) for further information.  
MGI:221354  
Seq primer: ETPRimer  
High quality sequence stop: 423.

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BASE COUNT      /lab_host="DH10B (ampicillin resistant)"
131 a          154 c          144 g          109 t
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## ORIGIN

Query Match 36.4%; Score 95; DB 34; Length 538;  
 Best Local Similarity 73.4%; Pred. No. 3.20e-111;  
 Matches 157; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

Db 12 CCCAGTCATGAGAGGTTCTCTGCGCCACCTGTTGGTGGCTGCTGTGGAGG 71  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 42 CCCAGCATGAGAGGCTCTCTGTCACGAGCTGTGGTGTGCTGCTGTGGAGG 101  
 Db 72 CAGCGGCACTCC-AGCACACCAAGTCCCTGTCAAGACCAAGGCAAAATGTGTTCCCTG 130  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 102 CAGGTGAGTCCAGCACCCAGGTCCTATCAAGATGCAAGCAACTGGCCCTCAG 161  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 131 AACGAGAACAGAGAGGTCGTGGATACTAGAGCCCTGTGAGCTCTTGAAGAGCAACC 190  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 162 AGCAGAGACCCAGAGAGGCTGGGGCGCCCTGTGTGTGAGACCTCCGAGAGAGCAGACC 221  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 191 AGCTGGGGCCACTGCTCTCTGAACCCAAACAGAA 224  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 222 AGCTGTGTGTGCTGTCTCTCTGTCAGAGCCGAA 255

RESULT 15  
 LOCUS AA030782 557 bp mRNA EST  
 DEFINITION m15c06.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone  
 IMAGE:463594 5' similar to gb:U28486 Mus musculus uterine-specific  
 prolone-rich acidic protein (MOUSE), mRNA sequence.

ACCESSION AA030782  
 NID g1500770  
 VERSION AA030782.1 GI:1500770  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 557)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT On May 18, 1995 this sequence version replaced gi:811026.

Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LIND : contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:277410  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 469.  
 Location/Qualifiers

## FEATURES

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 /organism="Mus musculus"  
 /note="Vector: pT73D (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dt) primer [5',  
 TGTACCAATCTGAAGTGGAGCGCGCATTTTGTGTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. RNA was kindly provided by  
 Dr. Minoru Ko (Wayne State University)."  
 /db\_xref="taxon:10090"

/map="6"  
 /clone="IMAGE:463594"  
 /clone\_lib="Soares mouse p3NMF19.5"  
 /dev\_stage="19.5 dpc total fetus"  
 /lab\_host="DH10B (ampicillin resistant)"

BASE COUNT 143 a 155 c 148 g 111 t

Query Match 36.4%; Score 95; DB 35; Length 557;  
 Best Local Similarity 73.4%; Pred. No. 3.20e-111;  
 Matches 157; Conservative 0; Mismatches 56; Indels 1; Gaps 1;

Db 21 CCCAGTCATGAGAGGTTCTCTGCGCCACCTGTTGGTGGCTGCTGTGGAGG 80  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 42 CCCAGCATGAGAGGCTCTCTGTCACGAGCTGTGGTGTGCTGCTGTGGAGG 101  
 Db 81 CAGCGGCACTCC-AGCACACCAAGTCCCTGTCAAGACCAAGGCAAAATGTGTTCCCTG 139  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 102 CAGGTGAGTCCAGCACCCAGGTCCTATCAAGATGCAAGTCAAACTGGCCCTCAG 161  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 140 AACGAGAACAGAGAGGTCGTGGATACTAGAGCCCTGTGAGACCTTGAAGAGCAACC 199  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 162 AGCAGAGACCCAGAGAGGCTGGGGCGCCCTGTGTGTGAGACCTCCGAGAGAGCAGACC 221  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 200 AGCTGGGGCCACTGCTCTCTGAACCCAAACAGAA 233  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 222 AGCTGTGTGTGCTGTCTCTCTGTCAGAGCCGAA 255

Search completed: Tue Aug 3 18:12:32 1999  
 Job time : 650 secs.



24758 #5

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Distribution rights by Oxford Molecular Ltd

MPsrch_nn	n.a.	-	n.a.	database search, using Smith-Waterman algorithm

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Run on: Tue Aug 3 20:11:15 1999; MasPar time 1127.82 Seconds
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Tabular output not generated.

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Title: >US-09-049-695-5
Description: (1-622) from US09049695.seq
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Perfect Score:	622
N.A. Sequence:	1 CTGGGATCAGCCACTGACAG.....TAACCCCGACAGGCGGGGA 622
Comp:	GACCTAGTGGTGACGTCG.....ATTGGGTCGTCCGGCCCT

Scoring table: TABLE default

Nmatch STD : Dbase 0; Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

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Post-processing: Minimum Match 0%
Listing first 45 summaries
```

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Database:      emb1-est58
1.00m Oct+10  3.00m Oct+11  3.00m Oct+17  4.00m Oct+18  5.00m Oct+19
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Database: genbank-est111

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8:9b_est10 9:9b_est10 10:9b_est11 11:9b_est12 12:9b_est13
13:9b_est14 14:9b_est15 15:9b_est16 16:9b_est17
17:9b_est18 18:9b_est19 19:9b_est20 20:9b_est21
21:9b_est22 22:9b_est23 23:9b_est24
25:9b_est25 26:9b_est26 27:9b_est27 28:9b_est28
29:9b_est29 30:9b_est31 31:9b_est32 32:9b_est33 33:9b_est34
34:9b_est35 35:9b_est36 36:9b_est37 37:9b_gss1 38:9b_gss2
39:9b_gss3 40:9b_gss4 41:9b_gss5 42:9b_gss6

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Statistics: Mean 10.525; Variance 2.484; scale 4.236

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
c 1	513	82.5	534	14	AA502331	ne26t06.s1 NCI_CGAP_Co	0.00e+000
c 2	422	67.8	474	15	AA568450	nm25b08.s1 NCI_CGAP_Co	0.00e+000
c 3	385	61.9	389	21	A1017393	ou92t09.x1 NCI_CGAP_K1	0.00e+000
c 4	309	49.7	424	19	T818178	yd79c11.s1 Soares_feta	0.00e+000
c 5	304	48.9	501	14	AA503839	ne53a10.s1 NCI_CGAP_Co	0.00e+000
c 6	302	48.6	457	19	T85588	yd82t10.s1 Soares_feta	0.00e+000
c 7	288	44.3	351	19	T85589	yd82t10.s1 Soares_feta	0.00e+000
c 8	267	42.9	378	19	T72043	yc53b05.s1 Strataene	0.00e+000
c 9	266	42.8	374	11	AA299977	ES11598 Uterus_tumor	0.00e+000
c 10	212	34.1	357	19	T86494	yd81n10.r1 Soares_feta	0.00e+000

C	11	184	29.6	188	11	AA535186	EST396634	Epilidymus	Ho	3.65e-18
	12	139	22.3	139	14	AA551860	ng91c09.3	NCI_C6AP	C	1.3e-18
	13	103	16.6	560	26	AT339147	mc19b06.y1	Soares	mo	4.21e-12
	14	103	16.6	590	25	AT332091	mf13b06.y1	Soares	mo	4.21e-12
	15	100	16.1	578	34	W66494	mb17h10.r1	Soares	mo	3.85e-11
	16	100	16.1	600	33	W10974	ma46d11.r1	Soares	mo	3.85e-11
	17	100	16.1	1114	34	W29238	mb56e09.r1	Soares	mo	3.85e-11
	18	98	15.8	538	34	W03342	mc25c10.r1	Soares	mo	7.65e-11
	19	98	15.8	557	35	AA030782	ml15c06.r1	Soares	mo	7.65e-11
	20	98	15.8	565	34	W66411	mb33g01.r1	Soares	mo	7.65e-11
	21	98	15.8	571	35	AA060119	mf13b06.r1	Soares	mo	7.65e-11
	22	96	15.4	418	35	AA020563	mb33g01.r1	Soares	mo	1.49e-11
	23	96	15.4	431	35	W08257	mb44b07.r1	Soares	mo	1.49e-11
	24	96	15.4	478	17	AA691263	vb23h09.r1	Soares	mo	1.49e-11
	25	96	15.4	510	20	AA871980	vg47h04.r1	Barstead	bo	1.49e-11
	26	93	15.0	508	20	AA871942	vg42h10.r1	Barstead	bo	1.24e-10
	27	93	15.0	572	20	AA871332	vg43a08.r1	Barstead	bo	1.24e-10
	28	91	14.6	379	33	W14887	mb29f05.r1	Soares	mo	2.31e-10
	29	91	14.6	497	33	W17866	mb33h05.r1	Soares	mo	2.31e-10
	30	91	14.6	543	35	AA060392	mf58b05.r1	Soares	mo	2.31e-10
	31	91	14.6	586	20	AA871263	vg33b08.r1	Barstead	bo	2.31e-10
	32	89	14.3	463	33	W17574	mb14f10.r1	Soares	mo	4.20e-99
	33	88	14.1	498	20	AA870378	vg44f10.r1	Barstead	bo	1.78e-97
	34	76	12.2	423	33	W20636	mb55h09.r1	Soares	mo	3.64e-78
	35	75	11.3	212	35	AA038591	ml55h09.r1	Soares	mo	1.12e-68
	36	62	10.0	366	20	F23035	SCG19a06	Porcine	small	3.02e-55
	37	62	10.0	485	16	AA671877	vg51d08.r1	Barstead	mo	3.02e-56
	38	62	10.0	252	17	AA754459	g75NI187	Rice	Immature	3.48e-55
C	39	59	9.6	534	16	AA969080	vb23e02.r1	Barstead	mo	1.24e-48
	40	49	7.9	540	34	W29850	mc07h12.r1	Soares	mo	9.26e-37
	41	48	7.7	257	17	AA754458	g75NI1784	Rice	Immature	2.62e-35
C	42	48	7.7	242	17	AA754459	g75NI1787	Rice	Immature	2.62e-35
	43	48	7.7	456	20	AA871485	vg36a07.r1	Barstead	bo	2.62e-35
	44	47	7.6	492	26	AA415324	mb16g01.r1	Soares	mo	7.28e-34
C	45	45	7.2	403	16	AA688510	vg35f07.r1	Barstead	mo	5.30e-31

## ALIGNMENTS

RESULT 1  
 LOCUS AA502331 534 bp mRNA  
 DEFINITION ne6h06.81 NCI\_CGAP\_C03 Homo sapiens cDNA clone IMAGE:598523 3'  
 similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN. ;, MRI  
 sequence.  
 ACCESSION AA502331  
 NID 92237298  
 VERSION AA502331.1 GI:2237298  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 534)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT On Sep 12, 1996 this sequence version replaced gi:1407178.

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,  
M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arraying: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/dbdp/image/image.html](http://www.bio.llnl.gov/dbdp/image/image.html)  
Insert Length: 690 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 398

FEATURES	Location/Qualifiers
source	1. .534

`/Organism:"Homo sapiens"`  
`/note="Vector: p7713-Pac (Pharmacia) with a modified`  
`polylinker: site.1: Not I; Site.2: Eco RI; 1st strand cDNA`  
`was prepared from 12 pooled bulk tumor samples and primed`  
`with a Not I - oligo(dT) primer. Double-stranded cDNA was`  
`ligated to Eco RI adaptors (Pharmacia), digested with Not`  
`I and cloned into the Not I and Eco RI sites of the`  
`modified p7713 vector. Library went through one round of`  
`normalization.`

```

/ad_xref="taxon:9606"
/clone="IMAGE:898523"
/clone_lib="NCI_CGAP_C03"
/sex="pooled"
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/lab_host="DH10B"

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BASE COUNT	80 a	160 c	178 g	115 t	1 others
ORIGIN					

Query Match	82.5%;	Score 513;	DB 14;	Length 534;
Best Local Similarity	98.3%;	Pred. No. 0.00e+00;		
Matches 526;	Conservative	0;	Mismatches 8;	Indels 1;
			Gaps 1;	

Db	1	TCGCGGCTCTGGGGTTATTATTGTCTAGTGGGGCAGGGTAGGGAGGGTCCAGTCCCA	60
CP	622	TCGCGGCTCTGGGGTTATTATTGTCTAGTGGGGCAGGGTAGGGAGGGTCCAGTCCCA	563
Db	61	ACAGCCTGGGCTTTGGGACAGGGGGGGGGAGTATGGCCCCCTGAGGCTTACTGGGGGT	120
CP	562	ACAGCCTGGGCTTTGGGACAGGGGGGGGGAGTATGGCCCCCTGAGGCTTACTGGGGGT	503
Db	121	GGTAGATGTGTCTTGTGCTTCCTCCGGTCCGAGAGACCTGTGTGATTGGCATCACCC	180
CP	502	GGTAGATGTGTGCTTGTGCTTCCTCCGGTCCGAGAGACCTGTGTGATTGGCATCACCC	443
Db	181	ACAACGGGGGCTCTCTCTCGCCCTTGGTCTCTCAGGGGAGGGTGTAGAGGCTGTAT	240
CP	442	ACAACGGGGGCTCTCTCTCGCCCTTGGTCTCTCAGGGGAGGGTGTAGAGGCTGTAT	383
Db	241	GGTGGGGCTCGGGACTCAGGACAGGGCCAGGGTGTCTCTGGTCTCCATCCAGGCTTGG	300
CP	382	GGTGGGGCTCGGGACTCAGGACAGGGCCAGGGTGTCTCTGGTCTCCATCCAGGCTTGG	323
Db	301	TGCGTGAAGATGGGGGCCCTGCGCTGACCTGTGGCTTCTCTCGGTGTCTAAAGTT	360
CP	322	TGCGTGAAGATGGGGGCCCTGCGCTGACCTGTGGCTTCTCTCGGTGTCTAAAGTT	263
Db	361	TGCGCTTCTGGACAGGGAAACAGCACACAGTGGTGTGCTTCTCCGAGGCTCCACCA	420
CP	262	TGCGCTTCTGGACAGGGAAACAGCACACAGTGGTGTGCTTCTCCGAGGCTCCACCA	203
Db	421	CAGGGGGCCCCCAGGC-TTCTCTTGGGTCTGCTCTGTGAGNGCAGTGTGGACTTGCATCT	479
CP	202	CAGGGGGCCCCCAGGCCTTCTCTGGGTCTGCTCTGTGAGNGCAGTGTGGACTTGCATCT	143
Db	480	TGATAGGGAATTTGGTGTGGGATGCACCTGCTCCACACAAAGAAAAACAAC	534
CP	142	TGATAGGGAATTTGGTGTGGGATGCACCTGCTCCACACAAAGAAAAACAAC	88

RESULT	2				
LOCUS	AA568450	474 bp	mRNA	EST	09-SEP-1997
DEFINITION	nm25b08.s1 NCI-CGAP_Col0 Homo sapiens cDNA clone IMAGE:1061175 3', similar to TR:0899433 G899433 PROLINE-RICH ACIDIC PROTEIN. ;, mRNA sequence.				
ACCESSION	AA568450				
NID	92341504				
VERSION	AA568450.1	GI:2341504			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	(bases 1 to 474)	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a>	National Cancer Institute, Cancer Genome Anatomy Project (CGAP)	
		Tumor Gene Index		
		Unpublished (1997)		
		On Sep 12, 1996 this sequence version replaced q1:1402127.		

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck  
M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/dbfp/image/image.html](http://www-bio.llnl.gov/dbfp/image/image.html)

Insert Length: 651      Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 197.

FEATURES	Location/Qualifiers
source	1. .474

/organism Homo sapiens". Vector: pT73D-Pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I and Eco RI adaptor (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares). "

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/clone="IMAGE:1061175"  
/clone_lib="NCI_CGAP_Co10"  
/tissue_type="colon tumor RER+"  
/lab_host="DH10B"
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ORIGIN				

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Query Match      67.8%; Score 422; DB 15; Length 474;
Best Local Similarity 98.7%; Pred. No. 0.00e+00;
Matches 453; Conservative 0; Mismatches 1; Indels 5; Gaps 5;
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Db	18	CCGGCCGCTGCTGGGGTTTATTGTCTAGCTGGGCGAGGGTGGGAGG-CCGAGTCCAA	76
Cp	621	CCCGGCTGCTGGGGTTATTGTCTAGCTGGGCGAGGGTGGGAGGTTCCAGTCCAA	56
Db	77	CAGCTGGGCGCTTGGGACAGGGGCGGCGAGTGTGCCC-TGGAGCCCTACTGGGGTG	13
Cp	561	CAGCTGGGCGCTTGGGACAGGGGCGGCGAGTGTGCCCCGGAGCCCTACTGGGGTG	50
Db	136	GTAGTGTGGCTTGGCTTCTCCGTCCAGGACGACCTGTGTGATTTGGCATACCCA	19
Cp	501	GTAGTGTGGCTTGGCTTCTCCGTCCAGGACGACCTGTGTGATTTGGCATACCCA	44
Db	196	CAACCGGGGCGCTTCCTCGCCCTGGTCTCTCTCAAGGGGAGGGTGTACAGGCTGTATG	25
Cp	441	CAACCGGGGCGCTTCCTCGCCCTGGTCTCTCTCAAGGGGAGGGTGTACAGGCTGTATG	38
Db	256	GTCGGGCTCGGGACTCAGGACAGCGGCCAGGATTCCTCGATCCATCCAGGCGTTGGT	31
Cp	381	GTCGGGCTCGGGACTCAGGACAGCGGCCAGGATTCCTCGATCCATCCAGGCGTTGGT	32
Db	316	GCTGTGAAGAAATGGGCCCCCTGCTTGACCTGTGTGCTTCTCTCAAGGNGTCAAGAG	37
Cp	321	GCTGTGAAGGA-TGGGGCCCCCTGCGCTTACCTC-GTGGCTTCTCTC-GGTGTCAAGAG	26
Db	376	TTTGGGTTTCTGGACAGGGAACAGACACACACAGTGTGTCTCTTCGCGAGGCTTCAC	43

Cp 264 TTTCGGCTTCTGACAGGGAACACACCAGCTGTCCTTCTCCGAGGCTCCAC 205

Db 436 CACACGGGGCCCCAGGCTTCTGGGTCTGCTGA 474

Cp 204 CACACGGGGCCCCAGGCTTCTGGGTCTGCTGA 166

RESULT 3

LOCUS AT017393 389 bp mRNA EST 27-AUG-1998

DEFINITION ou92f09.x1 NCI\_CGAP\_kid3 Homo sapiens cDNA clone IMAGE:1635305 3' similar to TR:060874 Q06084 PROLINE-RICH ACIDIC PROTEIN. ; mRNA sequence.

ACCESSION AT017393

NID 93231729

VERSION AT017393.1 GI:3231729

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 389)

AUTHORS Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)

COMMENT On Jan 14, 1998 this sequence version replaced gi:1797858.

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.lnl.gov/bdrip/image/image.html

Insert Length: 466 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES

Source Location/Qualifiers

1..389

/organism="Homo sapiens"

/note="Organ: kidney; Vector: p7773D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

/db\_xref="taxon:9606"

/map="957E09"

/clone="IMAGE:1635305"

/clone\_lib="NCI\_CGAP\_kid3"

/lab\_host="DH10B"

BASE COUNT 51 a 114 c 137 g 87 t

ORIGIN

Query Match 51.9% Score 385; DB 21; Length 389;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 TCCGGGCTCTGGGATTATTTGTTAGTGGGCAAGGTAGGAGGCTCCAGTCCA 64

Cp 622 TCCGGGCTCTGGGATTATTTGTTAGTGGGCAAGGTAGGAGGCTCCAGTCCA 563

Db 65 ACAGCCTGGGCTTGGACAGGGCGGGGAGTGTATGGCCCTTGAGCCTTACTGGGGGT 124

Cp 562 ACAGCCTGGGCTTGGACAGGGCGGGGAGTGTATGGCCCTTGAGCCTTACTGGGGGT 503

Db 125 GGTAGATGTGCTGTGCTCTTCTCTCCGCTCCAGAGACACCTGGTATTTGGCATACC 184

Cp 502 GGTAGATGTGCTGTGCTCTTCTCTCCGCTCCAGAGACACCTGGTATTTGGCATACC 443

Db 185 ACAACCGGGGCTCTCTCTCCCTGTGCTCTCTCAGCGGAGGGTGTACAGGCTGTAT 244

Cp 442 ACAACCGGGGCTCTCTCTCCCTGTGCTCTCAGCGGAGGGTGTACAGGCTGTAT 383

Db 245 GGTGGGCTGGGAGCTAGACACAGGCCAGGGGTGCTGCTCATCCAGGCTTG 304

Cp 382 GGTGGGCTGGGAGCTAGACACAGGCCAGGGGTGCTGCTCATCCAGGCTTG 323

Db 305 TGCCTGGAAGATGAGGCCCCCTGCTGACCTGTGCTCTCTCTGCTGCTGCTGCT 364

Cp 322 TGCGTGAAGATGAGGCCCCCTGCTGACCTGTGCTCTCTCTGCTGCTGCTGCT 263

Db 365 TCGGCTTCTGGACAGGAGACAGCAC 389

Cp 262 TCGGCTTCTGGACAGGAGACAGCAC 238

RESULT 4

LOCUS T78178 424 bp mRNA EST 15-MAR-1995

DEFINITION yd79c11.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:114452 5' similar to contains PIR5 repetitive element ; mRNA sequence.

ACCESSION T78178

NID 6966687

VERSION T78178.1 GI:696687

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 424)

AUTHORS Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.

TITLE The Wasno-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

CONTACT: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 644  
High quality sequence steps: 403 Source: IMAGE Consortium, LINL  
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert length: 644 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 403.

FEATURES

Source Location/Qualifiers

1..424

/organism="Homo sapiens"

/note="Organ: liver and spleen; Vector: p7773D (Pharmacia) with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAGAAATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

/db\_xref="GDB:470669"

/db\_xref="taxon:9606"

/clone="IMAGE:114452"

/clone\_lib="Soares fetal liver spleen INFLS"

/sex="male"



SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 457) Hillier,L., Clark,N., Dubnue,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Patson,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Tevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R. The Mashu-Merck EST Project unpublished (1995)
TITLE	Contact: Wilson RK
JOURNAL	Washington University School of Medicine
COMMENT	444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 671 High quality sequence stops: 210 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 671 Std Error: 0.00 Seq primer:-21ml3 High quality sequence stop: 210. Location/Qualifiers 1..457 /organism="Homo sapiens" /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAATAAAGAATCTTTTGTTTTTTTT 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bernaldo." /db_xref="GDB:470403" /db_xref="taxon:9606" /clone="IMAGE:114786" /clone_lib="Soares fetal liver spleen lNfLS" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" BASE COUNT 73 a 121 c 146 g 106 t 11 others ORIGIN
Query Match	48.6%; Score 302; DB 19; Length 457;
Best Local Similarity	90.3%; Pred. No. 0.00e+00;
Matches	400; Conservative 0; Mismatches 30; Indels 13; Gaps 13;
Db	3 TCCGGCGCTGCTGGGGTTATTTCCTACCTGGGN-AGGTAGGGAGGNC-AATCCA 60       
Cp	622 TCCGGCGCTGCTGGGGTTATTTCCTACCTGGGCAGGAGGAGGATGCCAATCCA 563       
Db	61 ACAGCCTGGGCTTGAGACAGGCGGGGCACTGATGGCCCCCTGAGCCCTACTGGGGT 120       
Cp	562 ACAGCCTGGGCTTGAGACAGGCGGGGCACTGATGGCCCCCTGAGCCCTACTGGGGT 503       
Db	121 GGATAGATGTGATCTGTCTTCCTCCGGTCCAGAGCACCTGTGATTTGGCATACC 180       
Cp	502 GGATAGATGTGATCTGTCTTCCTCCGGTCCAGAGCACCTGTGATTTGGCATACC 443       
Db	181 ACAACGGGGGCTTNTCTTCGCTGGGTCTCTACGCGGAGGGGTGTAACAGGCTNCA 240       
Cp	442 ACAACGGGGGCTTNTCTTCGCTGGGTCTCTACGCGGAGGGGTGTAACAGGCTNCA 384       
Db	241 TGGTGGGANTAGAGACAGGCGCCAGAGGTTNTCTTCGTTNCACTCAGGCGCTT 300       
Cp	383 TGTTGGGCTCGAGACTAGAGACAGGCGCCAGAGGTTCTCTTCATCCAGG-CCTT 325       
Db	301 GTGTCTGAAAGATGGGGGCCCCCTGCTGAACCTGTGCTTCCTCGTGGTGA 360       

Cp	324	GGTGGCTGGAGGA-TGGG-CCCTGGCTGGAGCTGGCTTCT-CTGGGTGGTAA	268			
Db	361	AAATTGGGCTTCTTGGACAAGAACACAGCAACAACTGGTGTCTTTTCCGG	420			
Cp	267	GAGTTGGGCTT-CT-GGACAG-GGAAGA-CCACACACAGT-GTGTCTTCT-CCGG	214			
Db	421	AGCTTCAACAAAAAGGGGCC	443			
Cp	213	AGGCTCCACACAGGGGGCCCC	191			
RESULT	7	785588	351 bp	mRNA	EST	17-MAR-1995
LOCUS		y882940.r1	Soares fetal liver spleen	INFLS	Homo sapiens	CDNA clone
DEFINITION		IMAGE:114786	5', mRNA sequence.			
ACCESSION		785588				
NID		6713940				
VERSION		785588.1	GI:713940			
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
AUTHORS		Eutheria; Primates; Catarrhini; Homidae; Homo.				
		1 (bases 1 to 351)				
		Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,				
		Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,				
		Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,				
		Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and				
		Wilson, R.				
TITLE		The Wash-Merck EST Project				
JOURNAL		Unpublished (1995)				
COMMENT		Contact: Wilson RK				
		Washington University School of Medicine				
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
		Tel: 314 286 1800				
		Fax: 314 286 1810				
		Email: est@watson.wustl.edu				
		Insert Size: 671				
		High quality sequence stops: 241				
		Source: IMAGE Consortium, LNL				
		This clone is available royalty-free through LNL; contact the				
		IMAGE Consortium (info@image.lnl.gov) for further information.				
		Insert Length: 671				
		Std Error: 0.00				
		Seq primer: M13Rpl				
		High quality sequence stop: 241.				
FEATURES		Location/Qualifiers				
Source		1..351				
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		/note="Organ: Liver and Spleen; Vector: p17T3D (Pharmacia)				
		with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;				
		1st strand cDNA was primed with a Pac I - oligo(dT) primer				
		[5' AACTGAGAATTAATTAAGATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT				
		3'],				
		double-stranded cDNA was ligated to Eco RI adaptors				
		(Pharmacia), digested with Pac I and cloned into the Pac I				
		and Eco RI sites of the modified p17T3 vector. Library				
		went through one round of normalization. Library				
		constructed by Benito Soares and M.Fatima Bonaldo."				
		/db_xref="GDB:470403"				
		/db_xref="taxon:9606"				
		/clone="IMAGE:114786"				
		/clone_id="Soares fetal liver spleen INFLS"				
		/sex="male"				
		/dev_host="20 week-post conception fetus"				
		/lab_host="DH10B (ampicillin resistant)"				
BASE COUNT		76 a	100 c	107 g	64 t	4 others
ORIGIN						
		Query Match				
		Best Local Similarity 95.2%;				
		Matches 316; Conservative				
		46.3%; Score 288; DB 19; Length 351;				
		Pred. No. 0.00e+00;				
		0; Mismatches 13; Indels 3; Gaps 3;				
Db	5	GACATGAGAGGCTCTCTGGTGCACGAGCCGTGGTGTGCTGCTGTGGAGGACAGT	64			







TITLE Fraser, C.M. and Venter, J.C.  
Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence  
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)  
MEDLINE 96026280  
COMMENT On Apr 14, 1993 this sequence version replaced gi:837374.

Other ESTs: TNC104700  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi.html>)  
Seq primer: M13 Reverse.

# FEATURES

source Location/Qualifiers  
1..188  
/organism="Homo sapiens"  
/note="Organ: epididymis; Vector: pBluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI"  
/db\_xref="ATCC (Inhost):136917"  
/db\_xref="taxon:9606"  
/clone\_lib="Epididymus"  
/sex="male"  
/dev\_stage="adult"  
BASE COUNT 40 a 68 c 51 g 26 t 3 others  
ORIGIN

Query Match 29.6%; Score 184; DB 11; Length 188;  
Best Local Similarity 98.4%; Pred. No. 3 65e-266;  
Matches 184; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2 CCGGTTTGGGTGATGCCAATACAGAGTCTCTCTGGAGCCGAGGAAGACCAAGACCA 61  
|||||  
Qy 435 CCGGTTTGGGTGATGCCAATACAGAGTCTCTCTGGAGCCGAGGAAGACCAAGACCA 494  
|||||  
Db 62 CATCTACACCCCGAGTGGGCTCCAGGGGCATCTAGTCCCGCTGTCCAGAGCC 121  
|||||  
Qy 495 CATCTACACCCCGAGTGGGCTCCAGGGGCATCTAGTCCCGCTGTCCAGAGCC 554  
|||||  
Db 122 CAGGCTGTTGGAGTGGAGACCTCCCTACCTGCCCCAGCTAGAGAAATAAACACACCA 181  
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Qy 555 CAGGCTGTTGGAGTGGAGACCTCCCTACCTGCCCCAGCTAGAGAAATAAACACACCA 614  
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Qy 615 GCGCCGG 621  
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RESULT 12  
LOCUS AA551860 139 bp mRNA EST 04-SEP-1997  
DEFINITION ng01009.s1 NCI-CGAP\_Co3 Homo sapiens cDNA clone IMAGE:28144 3'  
sequence similar to TR:8899433 G889433 PROLINE-RICH ACIDIC PROTEIN.; mRNA  
ACCESSION AA551860  
NID G2322112  
VERSION AA551860.1 GI:2322112  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 139)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On Apr 14, 1993 this sequence version replaced gi:838020.  
COMMENT  
JOURNAL  
Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,  
M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arraying: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/BLNI at:  
[www.blo.bnl.gov/bnrlp/image/image.html](http://www.blo.bnl.gov/bnrlp/image/image.html)

# FEATURES

source Location/Qualifiers  
1..139  
/organism="Homo sapiens"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from 12 pooled bulk tumor samples and primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified pT73 vector. Library went through one round of  
normalization."  
/db\_xref="taxon:9606"  
/clone\_lib="NCI-CGAP\_Co3"  
/sex="pooled"  
/tissue\_type="colon"  
/lab\_host="DH10B"  
BASE COUNT 17 a 42 c 47 g 33 t  
ORIGIN

Query Match 22.3%; Score 139; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 1.13e-182;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGTGTAGATGTGATGTGCTCTCTCCGCTCCAGAGACACCTGATTTGGCATCA 60  
|||||  
Cp 505 GGTGTAGATGTGATGTGCTCTCTCCGCTCCAGAGACACCTGATTTGGCATCA 446  
|||||  
Db 61 CCCAACACCGGGGCTCTCTCCGCTCCAGAGACACCTGATTTGGCATCA 120  
|||||  
Cp 445 CCCAACACCGGGGCTCTCTCCGCTCCAGAGACACCTGATTTGGCATCA 386  
|||||  
Db 121 CATGTGGGCTGGGACT 139  
|||||  
Cp 385 CATGTGGGCTGGGACT 367  
|||||

RESULT 13  
LOCUS A1391147 560 bp mRNA EST 02-FEB-1999  
DEFINITION mcl6901.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone  
IMAGE:348720.5 similar to gb:028486 Mus musculus uterine-specific  
proline-rich acidic protein (MOUSE); mRNA sequence.  
ACCESSION A1391147  
NID G4217154  
VERSION A1391147.1 GI:4217154  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 560)  
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
Ritter, E., Kohn, S., Shin, T., Jackson, F., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
JOURNAL  
TITLE  
The WashU-NCI Mouse EST Project 1999



ACCESSION W36494  
 MID 91318399  
 VERSION W36494.1 GI:1318399  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 578)

AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT On Nov 29, 1993 this sequence version replaced gi:430545.

Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:216315

Seq primer: EMP1mer  
 High quality sequence stop: 401.

FEATURES  
 source Location/Qualifiers

1..578  
 /organism="Mus musculus"  
 /note="Vector: pT73D (Pharmacia) with a modified  
 polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5',  
 TGTTACCACTGAGTGGAGCGCGCCATTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. RNA was kindly provided by  
 Dr. Minoru Ko (Wayne State University)."  
 /db\_xref="taxon:10090"  
 /map="21"  
 /clone="IMAGE:334915"  
 /clone\_lib="Soares mouse p3NMF19.5"  
 /dev\_stage="19.5 dpc total fetus"  
 /lab\_host="DH10B (ampicillin resistant)"

BASE COUNT 143 a 155 c 159 g 114 t 7 others  
 ORIGIN

Query Match 16.1%; Score 100; DB 34; Length 578;  
 Best Local Similarity 72.2%; Pred. No. 3,85e-117;

Matches 171; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

Db 44 CCCCAGTCATGAAGAGTTTCTCCGCGCCACTGTTGTGCTGCTGCTGCTGAGAG 103  
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 QY 50 CCCCAGACATAGAGGCTCTCTCCGTCACCAAGCTGTGTGCTGCTGCTGAGAG 109  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 104 CAGCGCGAGTCC-AGCACACCAGTCCCTGTCAAGACCAAGCAACATGTCTCCCTG 162  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 110 CAGGTGCGAGTCCAGACCAAGTCCCTATCAAGATGCAAGACTGCGCCCTCAG 169  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 163 AACGAGAAACGAGAGGCTCTGGATCTAGAGCCCTGGAGCTCTTGAAGAAGACAACC 222  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 170 AGCAGGACCAAGAGAGCGCTGGGCGCCCTGTGTGAGAGCTCCGAGAAAGACGACC 229  
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 Db 223 AGCTGGGGCCACTGCTCTCTGACCAACGAAGCCTGCGAGTCCGAGAAAGC 279  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 230 AGCTGTGTGTCTCTTCCCTGTCCAGAAAGCCGAACCTTTGACCACCGAGAGAGC 286



Other\_ESTs: THC104472  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/ldb/hgi/hgi.html>)  
Seq primer: M13 Reverse.

FEATURES  
source  
Location/Qualifiers

1..274  
/organism="Homo sapiens"  
/note="Organ: uterus; Vector: pBluescript SK-; Site\_1:  
ECORI; Site\_2: XhoI"  
/db\_xref="ATCC (Inhost):192971"  
/db\_xref="taxon:9606"  
/clone\_lib="uterus tumor I"  
/dev\_stage="adult"  
BASE COUNT 60 a 80 c 84 g 46 t 4 others  
ORIGIN

Query Match 93.3%; Score 237; DB 11; Length 274;  
Best Local Similarity 97.9%; Pred. No. 0.00e+00;  
Matches 238; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 1 CACTGCACCTCCCTGAGACACTCTNTACAGAGAGCGGAGACCCAGACATGAGAGGCTCT 60  
Oy 12 CACTGCACCTCCCTGAGACACTCTNTACAGAGAGCGGAGACCCAGACATGAGAGGCTCT 71  
Db 61 CCTGTCACACGCTGGTGTGTCTCTGTGGAGGACAGTGCAGTCCAGACACCCAA 120  
Oy 72 CCTGTCACACGCTGGTGTGTCTCTGTGGAGGACAGTGCAGTCCAGACACCCAA 131  
Db 121 GGTCTCTATNAAGATGCAAGTNAACACTGCGCTCAGAGAGAGACCCAGAGAGGCTG 180  
Oy 132 GGTCTCTATCAAGATGCAAGTCAACACTGCGCTCAGAGAGAGACCCAGAGAGGCTG 191  
Db 181 GGGGGCCCTTTGGTGGAGCCTCCGAGAAAGAGACAGCAGTGTGTCTGTCCCTGT 240  
Oy 192 GGGGGCCCTTTGGTGGAGCCTCCGAGAAAGAGACAGCAGTGTGTCTGTCCCTGT 251  
Db 241 CCA 243  
Oy 252 CCA 254

LOCUS 2 172043 378 bp mRNA EST 01-MAR-1995  
DEFINITION y63b05.r1 Stratagene liver (#937224) Homo sapiens cDNA clone  
IMAGE:85329 5', mRNA sequence.  
ACCESSION T72043  
NID 9586564  
VERSION T72043.1 GI:686564  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 378)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,  
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
TITLE WashU-Merck EST Project  
JOURNAL Unpublished (1995)

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 291  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
Seq primer: M13Rpl  
High quality sequence stop: 291.

FEATURES  
source  
Location/Qualifiers

1..378  
/organism="Homo sapiens"  
/note="Organ: liver; Vector: pBluescript SK; Site\_1:  
ECORI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
Oligo dT. Hepatectomy from normal male caucasian. Average  
insert size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor  
sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5'  
CTCGAGTTTCTTTTCTTTTCTTTT 3"  
/db\_xref="GDB:502386"  
/db\_xref="taxon:9606"  
/clone\_lib="Stratagene liver (#937224)"  
/sex="male"  
/dev\_stage="49 years old"  
/lab\_host="SOLR cells (kanamycin resistant)"  
BASE COUNT 83 a 117 c 116 g 59 t 3 others  
ORIGIN

Query Match 89.8%; Score 228; DB 19; Length 378;  
Best Local Similarity 97.2%; Pred. No. 0.00e+00;  
Matches 244; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

Db 7 GAGAGGCACCTTCAAGTCTCCCTGAGACCTCTTACAGAGAGCGGAGACCCAGACATGAG 66  
Oy 5 GATAGGCACCTGCA-GCTCCCTGAGACCTCTTACAGAGAGCGGAGACCCAGACATGAG 63  
Db 67 AGGCTCTCTCTGGTCAACACCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 126  
Oy 64 AGGCTCTCTCTGTGTCAACACCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 123  
Db 127 GCACCCAAAGTCCCTTCAAGATGCAAGTCAACACTGCGCTCAGAGAGAGACCCAGAG 186  
Oy 124 GCACCCAAAGTCCCTTCAAGATGCAAGTCAACACTGCGCTCAGAGAGAGACCCAGAG 183  
Db 187 AAGGCTGGG-GGCGCTGT 245  
Oy 184 AAGGCTGGGCGCGCTGT 243  
Db 246 TTCCCTGTCCA 256  
Oy 244 TTCCCTGTCCA 254

LOCUS 3 178178 424 bp mRNA EST 15-MAR-1995  
DEFINITION yd79c11.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
IMAGE:114452 5' similar to contains PRS5 repetitive element ;, mRNA  
sequence.  
ACCESSION T78178  
NID 9596687  
VERSION T78178.1 GI:696687  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 424)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)

[illegible]





SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 501)
JOURNAL	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
	On Apr 14, 1993 this sequence version replaced gi:593200.
	Contact: Robert Strausberg, Ph.D.
	Tel: (301) 496-1550
	Email: Robert.Strausberg@nih.gov
	Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
	cDNA Library Preparation: M. Bento Soares, Ph.D.
	cDNA Library Arraying: Greg Lennon, Ph.D.
	DNA Sequencing by: Washington University Genome Sequencing Center
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLW at: <a href="http://www.bio.lnl.gov/bdnp/image/image.html">www.bio.lnl.gov/bdnp/image/image.html</a>
	Insert length: 585 Std Error: 0.00
	Seq primer: -40ml3 fwd. RT from Amersham
	High quality sequence stop: 190.
FEATURES	Location/Qualifiers
SOURCE	1..501
	/organism="Homo sapiens"
	/note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library went through one round of normalization."
	/db_xref="taxon:9606"
	/clone="IMAGE:901050"
	/clone_1bp="NCI_CGAP_Co3"
	/sex="pooled"
	/tissue_type="colon"
	/lab_host="DH10B"
BASE COUNT	62 a 148 c 165 g 126 t
ORIGIN	
	Query Match 55.1%; Score 14; DB 14; Length 501;
	Best Local Similarity 97.9%; Pred. No. 2.84e-184;
	Matches 143; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db	356 TGGACAGGAGCAGCAGCAGCAGCAGTGTGTCCTCTCTCGAGGCTCCAGCAGAGGCG 415
Cp	254 TGGACAGGAGCAGCAGCAGCAGCAGTGTGTCCTCTCTCGAGGCTCCAGCAGAGGCG 195
Db	415 CCCCAGCTCTCTCTGGGCTCCTGCTCTGAGGGCCAGTGTTCAGTCTGATCTGAAGG 475
Cp	194 CCCCAGCCTCTCTCTGGGCTCCTGCTCTGAGGGCCAGTGTTCAGTCTGATCTGAAGG 135
Db	476 ACCTTGGGCTCTGGAGCTGCACCTGC 501
Cp	134 ACCTTGGGCTCTGGAGCTGCACCTGC 109
LOCUS	8
RESULT	A1391147 560 bp mRNA EST 02-FEB-1999
DEFINITION	mc16g01.v1 Soares mouse p3NMF9.5 Mus musculus cDNA clone
	IMAGE:348720 5' similar to gb:U28485 Mus musculus uterine-specific
	proline-rich acidic protein (MOUSE);, mRNA sequence.
ACCESSION	A1391147
NID	94217154
VERSION	A1391147.1 GI:4217154
KEYWORDS	EST.
SOURCE	house mouse.

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Mus musculus	Elkayvora: Metazoa: Chordata: Craniata: Vertebrata: Mammalia;				
Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.					
1 (bases 1 to 560)					
Maria, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,					
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,					
Person, B., Swaller, T., Gibbons, M., Page, D., Harrey, N., Schurk, R.,					
Ritter, E., Koh, S., Ship, T., Jackson, Y., Cardenas, M., McCann, R.,					
Waterston, R. and Wilson, R.					
The WashU-NCI Mouse EST Project 1999					
Unpublished (1999)					
On Apr 14, 1993 this sequence version replaced g1:716760.					
Contact: Maria M/WashU-NCI Mouse EST Project 1999					
Washington University School of Medicine					
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA					
Tel: 314 286 1800					
Fax: 314 286 1810					
Email: mouseest@watson.wustl.edu					
This clone is available royalty-free through LNL: contact the					
IMAGE Consortium (info@image.llnl.gov) for further information.					
This read is a RESEQUENCE of a previously sequenced mouse clone					
This read has been verified (found to hit its original self in the					
correct orientation)					
Seq primer: -40RP from Gibco					
High quality sequence stop: 485.					
Location/Qualifiers					
1. 560					
/organism="Mus musculus"					
/note="Vector: p773D (Pharmacia) with a modified					
polylinker: Site 1: Not I; Site 2: Eco RI; 1st strand c					
was primed with a Not I - oligo(df) primer [5',					
TGTACCAATCTGAGGAGGAGGCGCCGCTTTTCTTTTCTTTT 3'},					
double-stranded cDNA was size selected, ligated to Eco I					
adapters (Pharmacia), digested with Not I and cloned into					
the Not I and Eco RI sites of a modified p773 vector					
(Pharmacia). Library went through one round of					
normalization to a Cot = 5. Library constructed by Benton					
Soares and M.Fatima Bonaldo. RNA was kindly provided by					
Dr. Minoru Ko (Wayne State University)."					
/db_xref="taxon:10090"					
/map="12"					
/clone="IMAGE:348720"					
/clone_id="Soares mouse p3JNM19.5"					
/dev_stage="19.5 dpc total fetus"					
/lab_host="DH10B (ampicillin resistant)"					
BASE COUNT	136 a	162 c	148 g	113 t	1 others
ORIGIN					
Query Match	39.0%	Score 99:	DB 26:	Length 560:	
Best Local Similarity 74.6%:	Pred. No. 2,44e-116:				
Matches 150: Conservative	0: Mismatches 51:	Indels 0:	Gaps 0:		
Db	44	CCCCAGTCATATAAAGGTTCTCTCTGCGCCACACTCTTTGGTGGCTGACACTGCTGGGAGG	103		
Qy	50	CCCCAGATGATGAGGAGGCTCTCTCTGTCACACACCTGGTGCTGCTCTCTGCGGAGG	109		
Db	104	CAGGCGCAGCTCCAGCACACACAGCTCTCTGTCAGACCAAGCAAGCAATGTGTCCTG	163		
Qy	110	CAGGTGCGAGTCCAGCACACCAAGTCCCTATCAAGATGCAAGTAAACATCGCCCTCAG	169		
Db	164	AACAGAAACAGAGAGAGGCTCTGGATACTAGACGCGCTTGAGAGGAGACAC	223		
Qy	170	AGCAGAGACCCAGAGAGGCGCTGGGGGCGCCCTGTGTGGAGACCTCCGGAGAGGACGACC	229		
Db	224	AGCTGGGGCCACTGCTTCTCTG	244		
Qy	230	AGCTGGTGGTGGTCTGTTCCCTG	250		
RESULT	9	A1323091	590 bp	MRNA	EST
LOCUS					
DEFINITION		m73B06.y1 Soares mouse p3JNM19.5 Mus musculus cDNA clone			23-DEC-1998

IMAGE:481715.5' similar to gb:U28486 Mus musculus uterine-specific  
proline-rich acidic protein (MOUSE);, mRNA sequence.

ACCESSION  
AI323091  
VERSION  
4057520  
KEYWORDS  
AI323091.1 GI:4057520  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus

REFERENCE  
1 (bases 1 to 590)  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE  
JOURNAL  
The Washu-HMI Mouse EST Project  
COMMENT  
On Apr 14, 1993 this sequence version replaced gi:693536.

Contact: Marra M/Mouse EST Project  
Washu-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:292459

This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 444.

#### FEATURES

source

1..590  
Location/Qualifiers

/organism="Mus musculus"  
/note="Vector: pT73D (Pharmacia) with a modified  
polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTACCAATCTGAAGTGGAGGCGCGCATTTTCTTTTCTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Dr. Minoru Ko (Wayne State University)."  
/db\_xref="taxon:10090"  
/map="between D1S1765 and UGB"  
/clone="IMAGE:481715"  
/clone.lib="Soares mouse p3MNF19.5"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"

BASE COUNT  
ORIGIN  
152 a 167 c 151 g 118 t 2 others

Query Match  
Best Local Similarity 74.6%; Pred. No. 2,44e-116;  
Matches 150; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Db 46 CCCAGTCATGAAGAGTTTCTCTGCGCCACCTGTTTGTGCTGCTACTGCTGTGGAGG 105  
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QY 50 CCCAGACATGAGGAGCTCTCTCTGTCACAGCCTGTGCTGTGCTGTGCGAGG 109  
Db 106 CAGCGCAGCTTCACAGACACAGGTCCCTGTCAAGACCAAGGCAAAACATGTGTTCCCTG 165  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 110 CAGGTGAGTCCACAGACCCCAAGGTCCTATCAAGATGCAAGTCAAAACATGCGCCCTGAG 169  
Db 166 AACGGAAGACGAGAGTCTGGGATAGAGCCCTGGAGCCTCTTGAAGAGACAAC 225  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 170 AGCAGGACCCAGAGAGGCTGGGGCCCGCTGTGTGTGAGACCTCCGAGAGAGACACACC 225

Db 226 AGCTGGGGCACATGCTTCTG 246  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 230 AGCTGTGTGCTGCTTCCCTG 250

RESULT 10  
LOCUS W36494 578 bp mRNA EST 11-SEP-1996  
DEFINITION mb7h10.r1 Soares mouse p3MNF19.5 Mus musculus cDNA clone  
IMAGE:334915.5' similar to gb:U28486 Mus musculus uterine-specific  
proline-rich acidic protein (MOUSE);, mRNA sequence.  
ACCESSION  
W36494  
NID  
GI318399  
VERSION  
W36494.1 GI:1318399  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus

REFERENCE  
1 (bases 1 to 578)  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE  
JOURNAL  
The Washu-HMI Mouse EST Project  
COMMENT  
On Nov 29, 1993 this sequence version replaced gi:430545.

Contact: Marra M/Mouse EST Project  
Washu-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:216315  
Seq primer: E7Primer

High quality sequence stop: 401.  
Location/Qualifiers

1..578

/organism="Mus musculus"  
/note="Vector: pT73D (Pharmacia) with a modified  
polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTACCAATCTGAAGTGGAGGCGCGCATTTTCTTTTCTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Dr. Minoru Ko (Wayne State University)."  
/db\_xref="taxon:10090"  
/map="21"  
/clone="IMAGE:334915"  
/clone.lib="Soares mouse p3MNF19.5"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"

BASE COUNT  
ORIGIN  
143 a 155 c 159 g 114 t 7 others

Query Match  
Best Local Similarity 75.1%; Pred. No. 1.84e-111;  
Matches 151; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

Db 44 CCCAGTCATGAAGAGTTTCTCTGCGCCACCTGTTTGTGCTGCACTGCTGGAGG 103  
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QY 50 CCCAGACATGAGGAGCTCTCTCTGTCACAGCCTGTGCTGTGCTGTGCGAGG 109  
Db 104 CAGCGCAGTTC-AGCACACAGGTCCCTGTCTCAAGACCAAGGCAAAACATGTGTTCCCTG 162

QY	110	CAGGTGACGTCCACAGCAAGCTCCCTATCAGATGGAACTCAAAACACTGCGCCCTAG	169
Db	153	AACAGAAACACAGAGAAGCTCTGGGATCTAGAGCCCTGGAGCCTCTTGAAGGACACAC	222
QY	170	AGCAGGACCCACAGAGAAGCCTGGGGCGCCCGTGTTGTGAGGCTCCGAGAAGGACAGCC	229
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RESULT	11		
LOCUS	W10974	600 bp	EST
DEFINITION	ma6ed1.1 Soares mouse p3jmf19.5 Mus musculus cDNA clone		01-OCT-1997
ACCESSION	W10974		
NID	g1285279		
VERSION	W10974.1	GI:1285279	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 600) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Giesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.		
TITLE	The Mashu-HMI Mouse EST Project		
COMMENT	Unpublished (1996)		

WashU-HMM Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watsn.wustl.edu  
 This clone is available royalty-free through LINL : contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI: 204365  
 Seq primer: ETPrimer  
 High quality sequence stop: 477.  
 Location/Qualifiers  
 1. .600

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polylinker: Site_1: Not I; Site_2: Eco RI; 1st strand CDNA
was primed with a Not I oligo(dT) primer 15',
TGTATCCATCTGAAAGTGGAGCGCCCATTTTATTTTATTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (pharmacla), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(pharmacla). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
/db_xref="taxon:10090"
/clone="IMAGE:313749"
/clone_lib="Soares mouse p3MNF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"

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Best Local Similarity	75.1%	Pred. No.	1.84e-11	
Matches	151	Conservative	0	Mismatches 49
			Indels	1
			Gaps	1

Db 27 CCCACGATGAGAGGTTCTCTCGCCACCTGTTTGTTGGTCCACTGCTGTGGAGG 86

QY	50	CCCCAGACATGAGGAGGCTCTCTCTCTGTCACCCAGCCTGGTGGTTGTGTGCTGCTGTGGGAGG	109
Db	87	CAGGCGGAGTCC - AGCAGCACAGTGTCCCTGTCTAAGACCCAAAGCAAAATGTGTTCCTG	145
QY	110	CAGGTGGAGTCCAGGACCCCAAGTGTCCCATTAAGATGCAAACTGGCCCTTAG	169
Db	146	AACGAGAAACAGAAAGGTGTGGATACTAGAGCCCTGAGGCTCTTTAAAGAGCAACC	205
QY	170	AGCAGGACCCAGAGAAAGGCTTGGGGGCCCTGTGTGTGGAGCTTCGGAGAGGACGACC	229
Db	206	AGCTGGGGCCACTGCTTCTTG	226
QY	230	AGCTGTTGTTGCTGTTCCCTG	250

LOCUS	12			
DEFINITION	w29238	1114 bp	mRNA	EST
ACCESSION	mb96609.f1	Soares mouse p3MNF9.5 Mus musculus cDNA clone		11-SEP-1996
NID	IMAG:33728.5	similar to gb:U28486 Mus musculus uterine-specific		
VERSION	p3309520	proline-rich acidic protein (MOUSE) ; mRNA sequence.		
KEYWORDS	w29238.1	GI:1309520		
SOURCE	EST.			
ORGANISM	house mouse.			
REFERENCE	Mus musculus			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	1 (bases 1 to 1114)			
	Marric,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.			
	Gaisel,S., Kucaba,T., Lacy,M., Le,M., Martin,U., Morris,M.,			
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,			
	Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and			
	Waterson,R.			
TITLE	The MashU-HMI Mouse EST Project			
JOURNAL	Unpublished (1996)			
COMMENT	On Apr 14, 1993 this sequence version replaced gi:785474.			

Contact: Marra M/Mouse EST Project  
 WashU-HHMT Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel.: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:218688  
 Seq primer: E7P1primer  
 High quality sequence stop: 388.  
 Location/Qualifiers  
 1..1114

FEATURES  
 SOURCE

/note=vector: pT73D (Pharmacia) with a modified  
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 was primed with a Not I - 0190(ct) primer [5']  
 TGTACCATCTGAGTGGAGCGGCCCATTTTCTTTTCTTTTC 3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Fatima Bonaldo. RNA was kindly provided by  
 Dr. Minoru Ko (Wayne State University).

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/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT      245 a      217 c      420 g      215 t      17 others

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/organism="Mus musculus"  
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 polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5].  
 TGTTACCAATGTGACGACGACGGCGGCAATTTTTTTTTTTT 3'),  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT713 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. RNA was kindly provided by  
 Dr. Minoru Ku (Wayne State University)."  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:349554"  
 /clone\_lib="Soares mouse p3NNF19.5"  
 /dev\_stage="19.5 dpc total fetus"

Contact: Mairia M/Mouse EST Project  
 WashU-HIMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LMN ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:277410  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 469.  
 Location/Qualifiers  
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Dr. Minoru Ko (Wayne State University).
/db_xref="taxon:10090"
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/clone="IMAGE:453594"
/clone.lib="Soares mouse P3NNE19.5"
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BASE COUNT
143 a 155 c 148 g 111 t
BRIGGIN

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Query Match	37.08;	Score 94;	DB 35;	Length 557;
Query Match	37.08;	Score 94;	DB 35;	Length 557;

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Matches 150; Conservative 0; Mismatches 50; Indels 1; Gaps 1;
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D <sub>b</sub>	21	CCCCAGTCATCAAAAGGTTTCTCGGGCACCCTTTTGAGGTGCACACTGCTGTGGGAG	80
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D <sub>b</sub>	81	CAGGCGCACCTCC-AGCACACCAGGTGCCCTGTCAAGACCAAAGGCAACAATGTGTTCCCTG	138
O <sub>y</sub>	110	CAGGTGCAGTCCCAGCACACCACAAGGTHCCCTATCAAGATGAAGTAGCAACACATGCGCCTCAG	168
D <sub>b</sub>	140	AACAGGAAAACAGAGAAGTCTCTGGGATACTAAAGCCCTTGGAGCCTCTTGA AAAAGCAAC	199
O <sub>y</sub>	170	AGCAGGACCCGAGAAAGGCTCTGGGGCGCCCTGTGTGTGAGACCTCCGAGAGAAAGCAAC	228
D <sub>b</sub>	200	AGCTGGGCGCACCTGCTTCCTG	220
O <sub>y</sub>	230	AGCTGTGTGTCTGTCTCTG	250

RESULT	15	11 0000 1000
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DEFINITION mb83g11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone

proline-rich acidic protein (MOUSE);, mRNA sequence.

NID 91318315

**KEYWORDS** EST.

ORGANISM Mus musculus

Eutheria; Ro

AUTHORS  
Marta, M., H.

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Waterston, R.

JOURNAL Unpublished (1996)



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•  
•

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 WISE (TM)  
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 Distribution rights by Oxford Molecular Ltd

MPsrch\_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Aug 3 18:53:34 1999: MasPar time 1117.97 Seconds  
 1288.988 Million cell updates/sec

Tabular output not generated.

Title: >US-09-049-695-4  
 Description: (1-615) from US09049695.seq  
 Perfect Score: 615  
 N.A. Sequence: 1 AGCCACGTCGAGTCCTGAG.....AAACCCAGCAGCGCGGCA 615  
 Comp: TCGGTGACGTCGAGGAGACTC.....TTTGGGTGTCGCGCGCGCT

Scoring table: TABLE default  
 Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 2883791 seqs, 1171580779 bases x 2

Post-processing: Minimum Match 0%  
 Listing first 4% summaries

Database: emb1-est58  
 1:em-est10 2:em-est11 3:em-est17 4:em-est18 5:em-est2

Database: genbank-est111  
 8:gb-est1 9:gb-est10 10:gb-est11 11:gb-est12 12:gb-est13

13:gb-est14 14:gb-est15 15:gb-est16 16:gb-est17  
 17:gb-est18 18:gb-est19 19:gb-est20 20:gb-est21  
 21:gb-est22 22:gb-est23 23:gb-est24 24:gb-est25  
 25:gb-est26 26:gb-est27 27:gb-est28 28:gb-est29  
 29:gb-est30 30:gb-est31 31:gb-est32 32:gb-est33  
 33:gb-est34 34:gb-est35 35:gb-est36 36:gb-est37 37:gb-est38  
 38:gb-est39 39:gb-est40 40:gb-est41 41:gb-est42 42:gb-est43

Statistics: Mean 10.508; Variance 2.478; scale 4.240

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	512	83.3	534	AA502331	ne26h06.s1 NCI_CGAP_CO	0.00e+00
2	424	88.9	474	AA568450	nm25b08.s1 NCI_CGAP_CO	0.00e+00
3	384	62.4	389	AA101793	ou92f09.x1 NCI_CGAP_K1	0.00e+00
4	309	50.2	424	AA101793	yd79c11.r1 Soares feta	0.00e+00
5	303	49.3	501	AA503839	ne53a10.s1 NCI_CGAP_CO	0.00e+00
6	301	48.9	457	AA503839	yd82g10.s1 Soares feta	0.00e+00
7	288	46.8	351	AA503839	yd82g10.r1 Soares feta	0.00e+00
8	265	43.3	274	AA299777	EST12598 Uterus tumor	0.00e+00
9	265	43.1	378	AA299777	EST12598 Uterus tumor	0.00e+00
10	212	34.5	357	AA299777	yd81h10.r1 Soares feta	0.00e+00

Result	LOCUS	DEFINITION	ACCESSION	NID	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	AA502331	534 bp mRNA	ne26h06.s1 NCI_CGAP_CO3 Homo sapiens CDNA clone IMAGE7898233, similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN. ; mRNA	AA502331	92237298	GI:2237298	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	1 (bases 1 to 534)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Unpublished (1997)
1	AA502331.1	GI:2237298											On Sep 12, 1996 this sequence version replaced gi:1407178.

## ALIGNMENTS

EST396334 Epilidymus Ho	6.24e-183
ng01c09.s1 NCI_CGAP_CO	6.24e-183
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mc173b06.y1 Soares	2.71e-122
mb71h10.r1 Soares	2.51e-117
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mb46d11.r1 Soares	2.51e-117
mb56e09.r1 Soares	2.51e-117
mc25c10.r1 Soares	5.03e-114
mb15c06.r1 Soares	5.03e-114
mb39g11.r1 Soares	5.03e-114
mb73b06.r1 Soares	5.03e-114
mb51c09.r1 Soares	9.91e-111
mb44b07.r1 Soares	9.91e-111
vb12h09.r1 Barstead	9.91e-111
vb47h04.r1 Barstead	9.91e-111
vb42h10.r1 Barstead	8.35e-106
vb43a08.r1 Barstead	8.35e-106
mb29f05.r1 Soares	1.57e-102
mb33h03.r1 Soares	1.57e-102
mb58b05.r1 Soares	1.57e-102
vb33b08.r1 Barstead	1.57e-102
mb74f08.r1 Soares	2.88e-99
vb44f10.r1 Barstead	1.22e-97
mc16g01.r1 Soares	2.64e-78
mb15h09.r1 Soares	8.34e-69
SSC119806 Porcine small	2.33e-56
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97SN1787 Rice Immature	2.71e-55
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mc07h12.r1 Soares	7.57e-37
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vb36a07.r1 Barstead	2.15e-35
mc16g01.r1 Soares	6.01e-34
vb33f07.r1 Barstead	4.41e-31

Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,  
 M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arraying: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/dbip/image/image.html  
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/lab\_host="DH10B (ampicillin resistant)"  
BASE COUNT 89 a 119 c 133 g 75 t 8 others  
ORIGIN

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Best Local Similarity 92.0%; Pred. No. 0.00e+00;  
Matches 390; Conservative 0; Mismatches 23; Indels 11; Gaps 10;

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Oy 43 CCGAGCATGAGAGAGCTCTCTGTCACACAGCTGTGTGTCTGCTGTGGAGGC 102
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Db 61 AGGTGAGTCCCGACAGCCCAAGGTCCCTATCAAGATGCAAGTAAACACTGGCCCTACA 120
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Oy 103 AGGTGAGTCCCGACAGCCCAAGGTCCCTATCAAGATGCAAGTAAACACTGGCCCTACA 162
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Y 163 GCAGAGCCAGAGAAAGCTGGGCGCCGTGTGTGAGAGCTCCGAGAGAGAGACCA 222
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Oy 343 CCGTGGG-CGGTGTCT-GAGT-CCCGAGGCGGACCATGACAGTGTGTGTGTGTGTGT 398
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Oy 399 CTGAGAGAGAG-CCAGG--CGAGG-AGAGGCGCCGCTGTGTGTGTGTGTGTGTGTGT 452
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Db 420 AGGT 423
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Oy 453 AGGT 456
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RESULT 5  
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DEFINITION ne53a10.s1 NCI.GAP.Co3 Homo sapiens cDNA clone IMAGE:901050 3'  
similar to TR:G899433 G899433 PROLINE-RICH ACIDIC PROTEIN.; mRNA  
sequence.  
AA503839  
AA503839  
AA503839  
AA503839.1 GI:2238806  
EST.  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 501)  
NCI-GAP http://www.ncbi.nlm.nih.gov/ncigap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
On Apr 14, 1993 this sequence version replaced gi:693200.  
JOURNAL  
COMMENT

Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,  
M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-GAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

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Seq Primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 190.  
Location/Qualifiers

## FEATURES

source

1..501

/organism="Homo sapiens"  
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polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from 12 pooled bulk tumor samples and primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified p773 vector. Library went through one round of  
normalization."

/db\_xref="taxon:9606"  
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/tissue\_type="colon"

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ORIGIN

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Best Local Similarity 93.2%; Pred. No. 0.00e+00;  
Matches 478; Conservative 0; Mismatches 7; Indels 28; Gaps 2;

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Db 77 CAGCTGGGCTTGGAGACAGGCGGCGAGTGTGCGC-TGAGCCCTACTGGGGTG 135
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Oy 553 CAGCTGGGCTTGGAGACAGGCGGCGAGTGTGCGCCTTGGAGCTTACTGGGGTG 494
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Oy 493 GTAGATGTGTTGTTCTTCTCCGCTCCAGAGACCTGTGATTTGGATCACCA 434
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Db 196 CAACGGGGCTCTCTCTGCGCTGTCTCTAGGCGGAGGTGTGATGAGCTGTATG 255
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Oy 433 CAACGGGGCTCTCTCTGCGCTGTCTCTAGGCGGAGGTGTGATGAGCTGTATG 374
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Source	Organism	Human
REFERENCE	Human	Human
AUTHORS	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.	
TITLE	1 (bases 1 to 457)	
JOURNAL	Hillier, L., Clark, N., Duboue, T., Elliston, K., Hawkins, M., Holtan, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.	
COMMENT	The Mashu-Merck EST Project Unpublished (1995)	
FEATURES	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 671 High quality sequence stops: 210 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert length: 671 Seq primer: -21m3 High quality sequence stop: 210. Location/Qualifiers 1..457 /organism="Homo sapiens" /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACGTGAGAGATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo." /db_xref="Gene:470403" /db_xref="Locus:9606" /clone="IMAGE:114786" /clone_lib="Soares fetal Liver spleen LNLs" /sex="male" /dev_stage="20 week post conception fetus" /lab_host="DH10B (ampicillin resistant)" BASE COUNT 73 a 121 c 146 g 106 t 11 others ORIGIN	
Query Match	48.9%; Score 301; DB 19; Length 457;	
Best Local Similarity	90.3%; Pred. No.0.00e+00;	
Matches	399; Conservative 0; Mismatches 30; Indels 13; Gaps 13;	
Db	4 CCGGCTGCTGGGCTTATTTGCTAGTGGG-N-AGGTTAGGAGGGGNC-AGTCCCA 61	
Cp	613 CCGGCTGCTGGGCTTATTTGCTAGTGGG-N-AGGTTAGGAGGGGNC-AGTCCCA 554	
Db	52 CAGCTGGGCTTGGGAGAGGGGCGGAGTATGACCTTGGAGACCTTACCTGGGGTG 121	
Cp	553 CAGCTGGGCTTGGGAGAGGGGCGGAGTATGACCTTGGAGACCTTACCTGGGGTG 494	
Db	122 GTAGATGTGTTGTGCTTCTCCGCGGTCCAGAGACACCTGGTATTTGGCATACCA 181	
Cp	493 GTAGATGTGTTGTGCTTCTCCGCGGTCCAGAGACACCTGGTATTTGGCATACCA 434	
Db	182 CAACGGGGCTTCTCTGGCTGGGCTCTCTCAGCGGAGGGTGTACAGGCTTTCAT 241	
Cp	433 CAACGGGGCTTCTCTGGCTGGGCTCTCTCAGCGGAGGGTGTACAGGCTTTCAT 375	
Db	242 GGTGGGNTGGGANTCAGAGCAGGCGCCAGGCTTCTCGGTTTTCATCCAGGGCTTG 301	
Cp	374 GGTGGGNTGGGANTCAGAGCAGGCGCCAGGCTTCTCGGTTTTCATCCAGG-CTTG 316	
Db	302 GTGCTGGAAGGATGGGGCCCTGCTGGAACCTGTGGCTTTCTTCTGGGTGTCAA 361	

CP	315	GTGGCTGGAAAGA-TGGGG-CCCTGGCCCTGACCTCGTGGCTTCT-CTCGGTGGTCAAG	259
Db	362	ANTTTCGGCTTCTGTGACAAAGGAGACAGACACACACTTGTGTCCTTTTCCGGA	421
CP	258	AGTTTCGGCTT-CT-GGACAG-GGAGCA-GCACACACAGCT-GGTCTGCTTCT-CCGGA	205
Db	422	GCTTNCACAAAAAGGGGGCCC	443
CP	204	GGCTCCACACACAGGGGCCCCC	183
RESULT	7		
LOCUS		785588	351 bp mRNA EST 17-MAR-1995
DEFINITION		y882940.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone	
ACCESSION		IMAGE:114786 5', mRNA sequence.	
NID		T85588	
KEYWORDS		G713940	
VERSION		T85588.1	GI:713940
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
AUTHORS		Eutheria; Primates; Catarrhini; Homiidae; Homo.	
		1 (bases 1 to 351)	
		Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,	
		Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,	
		Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,	
		Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and	
		Wilson,R.	
TITLE		The WashU-Merck EST Project	
JOURNAL		Unpublished (1995)	
COMMENT			
		Contact: Wilson RK	
		Washington University School of Medicine	
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
		Tel: 314 286 1800	
		Fax: 314 286 1810	
		Email: est@watson.wustl.edu	
		Insert Size: 671	
		High quality sequence stops: 241 Source: IMAGE Consortium, LNL	
		This clone is available royalty-free through LNL; contact the	
		IMAGE Consortium (info@image.lnl.gov) for further information.	
		Insert Length: 671 Std Error: 0.00	
		Seq primer: M13Rpi	
		High quality sequence stop: 241.	
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		/organism="Homo sapiens"	
		/note="Organ: Liver and Spleen; Vector: p7T73D (Pharmacia)	
		with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;	
		1st strand cDNA was primed with a Pac I - Oligo(dT) primer	
		[5' AACTGGACAGATTAATTAAGATCTTTTTTTTTTTTTTT 3']	
		double-stranded cDNA was ligated to Eco RI adaptors	
		(Pharmacia), digested with Pac I and cloned into the Pac I	
		and Eco RI sites of the modified p7T73 vector. Library	
		went through one round of normalization. Library	
		constructed by Bento Soares and M.Fatima Bonaldo."	
		/db_xref="GDB:470403"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:114786"	
		/clone_id="Soares fetal liver spleen INFLS"	
		/sex="male"	
		/dev_host="20 week-post conception fetus"	
		/lab_host="DH10B (ampicillin resistant)"	
BASE COUNT		76 a 100 c 107 g 64 t 4 others	
ORIGIN			
		Query Match	46.8%; Score 288; DB 19; Length 351;
		Best Local Similarity	95.2%; Pred No. 0.00e+00;
		Matches	316; Conservative 0; Mismatches 13; Indels 3; Gaps 3;
Db	5	GACATGAGAGGCTCTCTCTGTGTCACGACCGCTGTGTGTGTCTGTGGAGGCAGCT	64

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QY 47 GACATGAGAGGCTCTCTGTGTCACACGCTGGTGGTGTGCTGTGTGGAGGACAGT 106
Db 65 GCAGTCCACACACCAAGGTCCTCATAGATGCACAAAGACTGGCCCTCAGACAG 124
QY 107 GCAGTCCACACACCAAGGTCCTCATAGATGCACAAAGACTGGCCCTCAGACAG 166
Db 125 GACCCAGAGAGGCTGTGGN-GGCCGTGTGTGAGAGCTCCGAGAGAGACGACAGCTG 183
QY 167 GACCCAGAGAGGCTGTGGGCGCCGTGTGTGAGAGCTCCGAGAGAGACGACAGCTG 226
Db 184 GTGTGCTGTGTCTCTGTCTCCAGAAAGCCAACTTTGACACAGAGAGAGAGAGAGT 243
QY 227 GTGTGCTGTGTCTCTGTCTCCAGAAAGCCAACTTTGACACAGAGAGAGAGAGT 286
Db 244 CAGGAGAGGAGGCTTCTCTCTCCAGAAAGCCAACTTTGAGATGAGAGAGAGAGAGT 303
QY 287 CAGGAGAGGAGGCTTCTCTCTCCAGAAAGCCAACTTTGAGATGAGAGAGAGAGT 346
b 304 GGCCTTTCTTAACTTCCNTAGCCGACCAT 335
QY 347 GGCCTGTCTCTGA-GTCCCG-AGCCCGACCAT 376
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RESULT 8 AA299977 274 bp mRNA EST 18-APR-1997
LOCUS EST12598 uterus tumor 1 Homo sapiens cDNA 5' end, mRNA sequence.
DEFINITION AA299977
ACCESSION g1952328
VERSION AA299977.1 GI:1952328
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 274)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Val,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitchugh,W.M., Fitchman,J.L., Georgagen,N.S.,
Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,T.A., Collins,E.J.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
```

```
TITLE Initial assessment of human gene diversity and expression patterns
JOURNAL based upon 83 million nucleotides of cDNA sequence
MEDLINE Nature 377 (6547 Suppl), 3-174 (1995)
COMMENT 96026280
On Sep 12, 1996 this sequence version replaced gi:1394394.
Other_ESTs: TRC104472
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018698056
Fax: 3018698423
```

```
FEATURES
source
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/cdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
1..274
/organism="Homo sapiens"
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/note="Organ: uterus; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhouse):192971"
/db_xref="taxon:9606"
/clone_lib="uterus tumor I"
/dev_stage="adult"
BASE COUNT 60 a 80 c 84 g 46 t 4 others
ORIGIN
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Query Match 43 3%; Score 266; DB 11; Length 274;
Best Local Similarity 97.8%; Pred. No. 0.00e+00;
Matches 268; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 4 CACTGAGCTCCCTGAGCACTCTNTACAGAGCGGGAGCCCGACATGAGAGGCTCT 63
Db 61 CCGTGTACACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 64 CCGTGTACACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 123
Db 121 GGTCCCTATNAGATGCAAGTAAACACTGGCCCTCAGAGCAGAGCCAGAGGCTGT 180
QY 124 GGTCCCTATNAGATGCAAGTAAACACTGGCCCTCAGAGCAGAGCCAGAGGCTGT 183
Db 181 GGGCGCCCGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 184 GGGCGCCCGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 243
Db 241 CCAGAGCCGAAACTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 274
QY 244 CCAGAGCCGAAACTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 277
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RESULT 9 T72043 378 bp mRNA EST 01-MAR-1995
LOCUS y63b05.t1 Striatum liver (#937224) Homo sapiens cDNA clone
DEFINITION IMAGE:85329 5', mRNA sequence.
ACCESSION T72043
VERSION g686564
KEYWORDS T72043.1 GI:686564
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 378)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevisan,E.,
Waterson,R., Williamson,A., Wohlmann,P. and Wilson,R.
WashU-Merck Est Project
Unpublished (1995)
```

```
TITLE JOURNAL
COMMENT Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estelw@wustl.edu
High quality sequence stops: 291
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: M13RPI
High quality sequence stop: 291.
Location/Qualifiers
1..378
/organism="Homo sapiens"
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FEATURES
source
/note="Organ: liver; Vector: pBluescript SK; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Hepatectomy from normal male caucasian. Average
insert size: 1.1 kb; uni-zap XR Vector; -5' adaptor
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CTCAGATTTTCTTTTCTTTT 3'
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/db_xref="taxon:9606"
/clone="IMAGE:85329"
/clone_lib="Stratagene liver (#937224)"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (Kanamycin resistant)"
BASE COUNT      83 a      117 c      116 g      59 t      3 others
ORIGIN
Query Match      43.1%; Score 265; DB 19; Length 378;
Best Local Similarity 97.9%; Pred. No. 0.00e+00;
Matches 280; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Db 11 AGCCACTTCAGCTCCCTGAGACCTCTCTACAGAGACGGGACCCAGACATGAGAGCC 70
QY 1 AGCCACTGCA-GCTCCTGAGCACTCTCTACAGAGACGGGACCCAGACATGAGAGCC 59
Db 71 TCCCTCTGTCACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 130
QY 60 TCCCTCTGTCACAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 119
Db 131 CCAAGTCCCTATCAAGATGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 190
QY 120 CCAAGTCCCTATCAAGATGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 179
Db 191 CTTGGG-CGGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 249
QY 180 CTTGGGCGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 239
Db 250 CTGTCAGAGCCGCAACTCTTGACACCGGAGAGAGCCAGCAGG 295
QY 240 CTGTCAGAGCCGCAACTCTTGACACCGGAGAGAGCCAGCAGG 285

RESULT 10      10      357 bp      mRNA      EST      17-MAR-1995
LOCUS      T86494
DEFINITION      Yb81h10. r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone
IMAGE:114691 5, mRNA sequence.
ACCESSION      T86494
NID      9714846
VERSION      T86494.1 GI:714846
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE      1 (bases 1 to 357)
AUTHORS      Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucada, T., Le, M., Lennon, G., Matra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
TITLE      The WashU-Merck EST Project
JOURNAL      Unpublished (1995)
COMMENT      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 716
This clone is available royalty-free through LNL.
High quality sequence stops: 232 Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 716 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stops: 232.
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location/Qualifiers
1..357
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/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: pT73D (pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACGTGAGAGATTAATTAACATCTTTTCTTTTCTTTT 3']
double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="GDB:470308"
/db_xref="taxon:9606"
/clone="IMAGE:114691"
/clone_lib="Soares fetal liver spleen 1NF1S"
/dev_stage="20 week post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT      72 a      101 c      112 g      64 t      8 others
ORIGIN
Query Match      34.5%; Score 212; DB 19; Length 357;
Best Local Similarity 92.6%; Pred. No. 0.00e+00;
Matches 263; Conservative 0; Mismatches 14; Indels 7; Gaps 6;

Db 1 AGGCTCCTCTGTCACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
QY 56 AGGCTCCTCTGTCACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 114
Db 61 AGCACCAGAGTCCCTATCAAGATGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 120
QY 115 AGCACCAGAGTCCCTATCAAGATGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 174
Db 121 GAACAGGGCCCTGAGGCGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 175 GAA--GGCTGTGGGGCGCCCT-GTGG-TGAGCCTCCGAGAGAGACAGCAGCAGTGTG 230
Db 181 TGTGTCTCCTGTTCAGAGCCGCAAACTGTGACACCGAGAGAGAGCCAGAGTGTGAG 240
QY 231 TGTGTCTCCTGTTCAGAGCCGCAAACTGTGACACCGAGAGAGAGCCAGAGTGTGAG 290
Db 241 GCAGGGGCCCATTCCTTTNAGGAGNCCAGAGCTGTGATTTGGA 284
QY 291 GCAGGGGCCCATTCCTT-CCAGG-CACCAAGGCTGTGATTTGGA 332

RESULT 11      11      188 bp      mRNA      EST      21-APR-1997
LOCUS      AA335186
DEFINITION      EST39634 Epiddlymus Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION      AA335186
NID      91987501
VERSION      AA335186.1 GI:1987501
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE      1 (bases 1 to 188)
AUTHORS      Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bull, C.J., Dee, N.H., Kirkness, E.F., Weinszock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geobaghen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Yi, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.-F., Wang, J., Xu, C., Yu, G.-L., Ruben, S.M.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
```

TITLE Fraser, C.M. and Venter, J.C.  
Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence  
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)  
MEDLINE 96026280  
COMMENT On Apr 14, 1993 this sequence version replaced gi:837374.  
Other ESTs: TNC104700  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlavage@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.

## FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
/note="Organ: epididymis; Vector: pBluescript SK-; Site\_1:  
ECORI; Site\_2: XhoI"  
/db\_xref="ATCC (Inhost):136917"  
/db\_xref="taxon:9606"  
/clone\_lib="Epididymus"  
/sex="male"  
/dev\_stage="adult"  
BASE COUNT 40 a 58 c 51 g 26 t 3 others  
ORIGIN

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Best Local Similarity 98.4%; Pred. No. 1,67e-260;  
Matches 184; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 427 CCGGTTTGGGTGATCCCAATNACCAAGTGTCTCTGGACCGGAGAACCAAGACCA 486  
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Db 62 CATCTACACCCCGATGAGGCTCCAGGGCCATCATGCCCCGCCCTGTCCCAAGGCC 121  
|||  
Qy 487 CATCTACACCCCGATGAGGCTCCAGGGCCATCATGCCCCGCCCTGTCCCAAGGCC 546  
|||  
Db 122 CAGGCTGTGGAGCTGGGACCTCCCTACCTGCCGCCCAAGTACAGCAATAACCCAGCA 181  
|||  
Qy 547 CAGGCTGTGGAGCTGGGACCTCCCTACCTGCCGCCCAAGTACAGCAATAACCCAGCA 606  
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Db 182 GGCCGGG 188  
|||  
Qy 607 GGCCGGG 613

RESULT 12  
LOCUS AA551860 139 bp mRNA EST 04-SEP-1997  
DEFINITION ng01c09.s1 NCI-CGAP\_C03 Homo sapiens cDNA clone IMAGE:928144.3,  
similar to TR:6899433 G899433 PROLIF-RICH ACIDIC PROTEIN.; mRNA  
sequence.  
ACCESSION AA551860  
NID 92322112  
VERSION AA551860.1 GI:2322112  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 139)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT On Apr 14, 1993 this sequence version replaced gi:838020.  
Contact: Robert Strausberg, Ph.D.

## FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from 12 pooled bulk tumor samples and primed  
with a Not I - 0190(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified pT73 vector. Library went through one round of  
normalization."  
/db\_xref="taxon:9606"  
/clone\_image="928144"  
/clone\_lib="NCI-CGAP\_C03"  
/sex="pooled"  
/tissue\_type="colon"  
/lab\_host="DH10B"  
BASE COUNT 17 a 42 c 47 g 33 t  
ORIGIN

Query Match 22.6%; Score 139; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 6.24e-183;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGTGTGATGTGGTCTGTGCTCTTCTCCGCTCCAGGACACCTGGTATTGGCATCA 60  
|||  
Cp 497 GGTGTGATGTGGTCTGTGCTCTTCTCCGCTCCAGGACACCTGGTATTGGCATCA 438  
|||  
Db 61 CCACAAACCGGGGCTCTCTCCCTCGCTGCTCCAGGAGGAGGTGTATAGGCTGT 120  
|||  
Cp 437 CCACAAACCGGGGCTCTCTCCCTCGCTGCTCCAGGAGGAGGTGTATAGGCTGT 378  
|||  
Db 121 CATGTGCGGCTGGGACT 139  
|||  
Cp 377 CATGTGCGGCTGGGACT 359

RESULT 13  
LOCUS AI391147 560 bp mRNA EST 02-FEB-1999  
DEFINITION mcl6g01.y1 Soares mouse p3NMf19.5 Mus musculus cDNA clone  
IMAGE:348720.5; similar to gb:U28486 Mus musculus uterine-specific  
proline-rich acidic protein (MUSE); mRNA sequence.  
ACCESSION AI391147  
NID 94217154  
VERSION AI391147.1 GI:4217154  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 560)  
AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,  
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.  
TITLE The WashU-NCI Mouse EST Project 1999  
JOURNAL Unpublished (1999)

COMMENT On Apr 14, 1993 this sequence version replaced gi:716760.

Contact: Maria M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watsn.wustl.edu

This clone is available royalty-free through LNL: contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 486.

FEATURES  
source location/Qualifiers  
1..560

/organism="Mus musculus"  
/note="Vector: pT73D (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTACCAATCTGAGTGGAGGCGCCGATTTTCTTTTCTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. RNA was kindly provided by  
Dr. Minoru Ko (Wayne State University)."  
/db\_xref="taxon:10090"  
/map="12"  
/clone\_lib="Soares mouse p3NM19.5"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"

BASE COUNT 136 a 162 c 148 g 113 t 1 others

Query Match 16.7%: Score 103; DB 26; Length 560;  
Best Local Similarity 71.7%: Pred. No. 2,71e-122;  
Matches 170; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Db 44 CCCAGTCATGAGAGGTTCTCTGCGCACCTGTTGGTGCACCTGCTGTGGAGG 103  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY .42 CCCAGCATGAGAGGCTCTCTGTCACACCTGTGGTGTGCTGTGTGGAGG 101  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 104 CAGGCGAGCTCCAGCACACCAAGTCCCTGTCAAGACCAAGCAACATGTTCCTG 163  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 102 CAGTGCAGTCCAGCACCCCAAGGTCCTATCAAGATGCAAGTCAACACTGGCCCTCAG 161  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 164 AACAGCAAGAGAGAGGTGGGATAGAGCCCTGGAGCCCTCTTGAAGAGCAAGC 223  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 162 AGCAGGACCCAGAGAGGCTGGGGCGCCGTGTGTGGAGCTCCGAGAGAGCAAGC 221  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 224 AGCTGGGGCCACTGCTTCTGTAACCAAGAGCCTGAGAGCTGCGAGAGAAAGC 280  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 222 AGCTGTGTGTGCTTCTGCTGTCAGAAAGCGGAACCTTGACCAACGAGAGAAAGC 278  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14  
LOCUS A1323091 590 bp mRNA EST 23-DEC-1998  
DEFINITION m73B06.v1 Soares mouse p3NM19.5 Mus musculus cDNA clone  
IMAGE:481715 5' similar to gb:U28486 Mus musculus uterine-specific  
proline-rich acidic protein (MOUSE);, mRNA sequence.  
ACCESSION A1323091  
NID 94057520  
VERSION A1323091.1 GI:4057520  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 590)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE The WashU-HMT Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT On Apr 14, 1993 this sequence version replaced gi:693536.

Contact: Maria M/Mouse EST Project  
WashU-HMT Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watsn.wustl.edu  
This clone is available royalty-free through LNL: contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:292459

This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 444.

FEATURES  
source location/Qualifiers  
1..590

/organism="Mus musculus"  
/note="Vector: pT73D (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTACCAATCTGAGTGGAGGCGCCGATTTTCTTTTCTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. RNA was kindly provided by  
Dr. Minoru Ko (Wayne State University)."  
/db\_xref="taxon:10090"  
/map="between D1S1765 and USB"  
/clone\_lib="Soares mouse p3NM19.5"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"

BASE COUNT 152 a 167 c 151 g 118 t 2 others

Query Match 16.7%: Score 103; DB 25; Length 590;  
Best Local Similarity 71.7%: Pred. No. 2,71e-122;  
Matches 170; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Db 46 CCCAGTCATGAGAGGTTCTCTGCGCACCTGTTGGTGCACCTGCTGGAGG 105  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 42 CCCAGCATGAGAGGCTCTCTGTCACACCTGTGGTGTGCTGTGTGGAGG 101  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 106 CAGGCGAGCTCCAGCACACCAAGTCCCTGTCAAGACCAAGCAACATGTTCCTG 165  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 102 CAGTGCAGTCCAGCACCCCAAGGTCCTATCAAGATGCAAGTCAACACTGGCCCTCAG 161  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 166 AACAGCAAGAGAGGTGGGATAGAGCCCTGAGAGCCTTGTGAAGAGCAAGC 225  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 162 AGCAGGACCCAGAGAGGCTGGGGCGCCGTGTGTGGAGCTCCGAGAGAGAGC 221  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 226 AGCTGGGGCCACTGCTTCTGTAACCAAGAGCCTGAGAGCTGCGAGAGAAAGC 282  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 222 AGCTGTGTGTGCTTCTGCTGTCAGAAAGCGGAACCTTGACCAACGAGAGAGC 278  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15  
LOCUS M36494 578 bp mRNA EST 11-SEP-1996  
DEFINITION mb71H10.r1 Soares mouse p3NM19.5 Mus musculus cDNA clone  
IMAGE:334915 5' similar to gb:U28486 Mus musculus uterine-specific  
proline-rich acidic protein (MOUSE);, mRNA sequence.

Search completed: Tue Aug 3 19:16:07 1999  
Job time : 1353 secs.

ACCESSION W36494  
 MID 91318399  
 VERSION W36494.1 GI:1318399  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 578)  
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.  
 TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT On Nov 29, 1993 this sequence version replaced gi:430545.

FEATURES  
 source  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:216315  
 Seq primer: EST primer  
 High quality sequence stop: 401.  
 Location/Qualifiers  
 1..578  
 /organism="Mus musculus"  
 /note="Vector: pRT3D (Pharmacia) with a modified  
 polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dt) primer [5',  
 TGTTACCAATGTGAAGTGGAGGCGCGCATTTTGTGTTTGTGTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pRT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. RNA was kindly provided by  
 Dr. Minoru Ko (Wayne State University)."  
 /db\_xref="taxon:10090"  
 /map="21"  
 /clone="IMAGE:334915"  
 /clone\_lib="Soares mouse p3NMF19.5"  
 /dev\_stage="19.5 dpc total fetus"  
 /lab\_host="DH10B (ampicillin resistant)"

BASE COUNT 143 a 155 c 159 g 114 t 7 others  
 ORIGIN

Query Match 16.38; Score 100; DB 34; Length 578;  
 Best Local Similarity 72.28; Pred. No. 2.51e-117;  
 Matches 171; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

DB 44 CCCCATCATGAGAGGTTCTCTGCGCCAGCTGTTGCTGCTGCTGCTGGAGG 103  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 42 CCCACACATGAGAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 101  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 DB 104 CAGGCGCAGTCC-AGCACACAGGTCCTGTCAGACCAAGCAACAATGTTCCCTG 162  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 102 CAGGTGACAGTCCAGCACCAGTCCCTATCAAGATGCAATCAACTGCGCTCAG 161  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 DB 163 AACAGGAACAGAGAGGTGTGGATAGAGCCCTGAGAGCCTCTTGAAGAGACACC 222  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 162 ACAGAGACCCAGAGAGGCTGCGGCCCGCTGTGTGTGAGCCTCCGAGAGAGACACC 221  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 DB 223 ACCTGGGCGCACTGTTCTTGAACCAACAGAGCCTGACGTGCGGAGAAAGC 279  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 222 AGCTGTGTGCTGTTCCCTGTCCAGAGCGAAGCTTGTACCAAGAGAGAAAGC 278